

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCCGAGGACCTGGAGCTCCGGCTCGGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGTGTG
CTGTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCCGGTGCCCGGGGCT
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCCTGTGTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCGTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCCAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGTCTGGGCCGTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCCGCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAAATGTGCCGGAATTACCCCTTTAAATTATTTCAGAAGGATGTCC
CGTGGAATAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTGCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCCGCATGGCCCAACTTGGTTATTGCACTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTGTCCAAATC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAAGTATAGGTTGTGGAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLPLLLLLPPAPEAAKPTPCHRCRGLVDKFNQGMVDTAKKNFGGNTAWEKTL SKYSESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLKVCSPGTYPGPDCLACQGGSGRQPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKCTCSGLTNRD CGCEVGVWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDS SCVCGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVVCPCDPGFEEEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEPLYLWIDAHQARVLIGFEEDILIVSEGG
MAPFTTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNITLQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGCGCGGGCCAGCCTGGG
 CCCAGCCCCACACCTTACCAGGGCCCAGGAGCCACCATGTTGGCGATGTCCACTGGGGCTAC
 TGCTGTTTGGTCCCGCTGGCTGGCCACTTGGCTCTGGGTGCCACGAGGGTCGTGGGCGCCGG
 GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
 GCAGGACCTGTGCTGCGCGGCGGTGCCGACGACTGTGCCCTGCCCTACCTTGGGCGCCATCT
 GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
 TGCTTCGGCGTGGCCACCCCTTTTCCCCCATGCCAAGGATGTATGCATGGAGGTCGTATCTA
 TCCAGTCTTGGGAACGTACTGGGACAACTGTAAACGGTTGCACCTGCCAGGAGAACAGGCAGT
 GGATGTGTGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
 GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGGCATTGCTACCGCCTGGGCACCA
 TCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGTGAACCCAGGGGAG
 GTGCTTCCACAGCCTTCGAGGCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
 CCAAGGCAACTGTGCGAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
 CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCAAGAACCTGCTGTCTTGTGAC
 ACCCACCAGCAGCAGGCTCGCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGCTCG
 CCGAGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
 CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
 CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
 TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
 AGCTTCGTGCTGGGCGTCTGGGGCCGCTGGGCATGGAGGACATGGGTCATCACTGAGCGTG
 CGGGCACCACGCGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
 GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGCGCAGGGGGCGCCAGGGCGCTAAT
 CCGGGCGCGGTTCCGTGACGCGAGCGCCCCCTGGGAGCCGCGGGCAGGCGAGACTGGCG
 GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTGGCCTGGGAAGAGCACAGCTCGAG
 ATCCCAGGCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTGTAGACAGGGTCTTGCTCCG
 TTGCCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACTCCGACTCCTGGGTTCA
 AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACACCTGGC
 TAATTTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTGCCAGGCTGGTTTTCGAAC
 CTTGGGCTCAAGCGGTCCACTGCCTCCGCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
 ACTGACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAA
 TAAACCAAAGTATTGATAAAAAAAA

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGCGCGGGCCAGCCTGGG

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
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ALPYLGAICYDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYYDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG



FIGURE 9

MTHRTTTWARTSRVAVTPTCATPAGPMPCSRLLPPLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHFNASLTMYVCTPVPHDPMPMALSRTPTTRQISSDT
DPPADGFSNPLCCCFHGPAPSTLNPVLRHLFPQEAFFAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTTCATGGCCTTCAACGCGGAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTTCCCCAACACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCAGTAGTCTGGGAGGCAGGGGCGAGGCCCTTGGGCCGCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCGTAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCGAGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAAGT
GAGTGTCACCCGTATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCTTGAGAGCAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTTGTGTTTTCAGGAAAAAGAAAGGGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCTGCTC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIKPSGKSKDCVFTEIVLE
NNYTAFQONARHEGWFMATFTRQGRPRQASRSRQNQREAHFIKRLYQGQLFFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTGTTGCTGTTTATTTTTTTTTCTTTTCTTTTTCCACCACATGTTATTTTAT
 TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCTCT
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC
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 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCAAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGACAAGTCCGGG
 GGATGGCCGTGAGGGAATTAATATGAATCTTTTGTCTGTCCCAACACGACCCCGGCTG
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 TCCAAACCTTAGCAGAAGCTACACGCTTCCAACCTCTACCACATCGAACTTCCACAGATTC
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 CATTTTGTGAATGATACTTCCATCAAGTCAAGTGGCTCTCTCTTCCACCGTGATGGCATA
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 TGTTTAGTCCCATGAGTGTCTTTAACTACCGCGCGGTAGAAGACCACTTTGTTGAGAGGC
 CACCACCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
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 AGGACAACCTCCATCTGGAGATGACAGAAACCAAGTTTTCAGATCGTCTCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTTACAGCTGCAGCCATTTACACCCCAATGGGGGCATTAATTA
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 CACACTCGTGTGTGCACATAAAGACACGAGATTACATTTGATAAATGTTACACAGATGCAT
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 CTATCTTTTCTATTCAAGTTAATTACAAACAGTTTTGTAACCTCTTGGCTTTTAAATCTT

0903740 071111

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRNDFVYCNERSLTSVPLGIP
EGVTVLVYLNHNQINNAGFPaelhNVQSVHTVYLYGNQLDEFFPMNLpKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNNSISTVGVEDGAFREAIslKLLfLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSlerLIvDGNLLtNKGIaEGTFshLTkLKEfSVIRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLtAFsNLrKLERLDISNNQLRMLtQGvFDNLSNLKQLTARNN
PWFCDCSIkwVTEWLKYIPSSLNVRGFMCQGPEQVRGMaVRELNMNLLSCTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNyRAVEDITCseATThASyLNNGSNTASSheQTtSHSMGSPfLLAGLIGGAVI FVLVVL
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNsILEMTETsFQIVSLNNDQLLKg
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

[illegible]

ACTTGGACGCAAGCCGGCGGCGGAGACAGAGGACGAGACAGAAAGCTGGGGCTCCGCTCTCGCCTCTCCGACGAGGAC
ATCCCGAGGAGACGCGCCGCCCTCTCGCGGAGGACAGAAAGCCGAGAGAAAGCCCGGTGGTGGTCCGCCCTGCC
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GCACATAGCTGGGCTGGCCATCAGATGTGCCGAAACATCGAATCTCAGAGACAGAGGGGCGCGGCCCTGAC
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AGAGAAGTGTGACCGGCCCACTTTGTGCAGCACTGGGACATCTGTGCCCACTTGTCACTCAAACTCCTGT
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CATAAATCATGAGACATATGACTTTGTGGAAACAGTTGGATTTTATACAAATATAAAATTCACCACTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARESRGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGDPDVT RVGLLQYGSSTVKNESFLKTFKRKSEVERAV
KRMRLHSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGR PQDSVAEVAAKARD
TGILIFAIGVGQVD FNTLKSIGSEPHEDHVFLVANFSQIETLT SVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDL CAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINRYCALNKP GC
EHECVNMESYYCRCHRGYTLD PNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGF LI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCP EGHVLRSDGKTCAKLDS CALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCBCL EGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISP KAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGE GARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEBELQEIASEPTNKHLYAEDFSTMD EISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
BEKHDQCCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTACGCGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCGGTGTGCGTCCCGCGGTGGCGCCCTGACTCCGTCCTCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCCAACCGGTTGCAG
GCGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACACGGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGTGGAGGGTCTCCAGGAGAAAAGACTCTGGCCCCTA
CAGCTGTCCGTGAATGTGAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTCCAGACTTTCTTTGCACCAGCATTAGATGTCAATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCAACCCTCAACCAATATCCCCCATCCCTGGTGGGTTTCTTCTCTGGCTTGAGCGG
CATGGTGCTGTGCCTGTGATGGTGCCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCACCCCTGACTCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTCCAGTCACTGAGTCTCCAGGC
CCCTTGATCTGTACCCCAACCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAAACTAACATGAAATATGTGTTGTTTTTCATTGTGCAATTTAAATAAAGATACATAA
TGTTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEFANDIKEDAIAPRTLFPWPKSSDTISKNGTL
SSVTSARALRPFHGPPRPALTPTPSLSSQALPSPRLPTTDGAHPQIPISIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 19

MKRLPLLVVFSTLLNCSYQNCCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCNTNTEGSSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCI
NINKTTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTLEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTCLMHTVEQATLRISSQSFQKTTEFDT
NSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSGIPLLS
SSDNFLKPKQNYDENSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPTDMNGSWSSGCELTYSNETHTSRCRNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGL
LHYFFLAFAWMCIIEGHIHLYLIVVGVIYKNGFLHKNFYIFGYLSPAVVVGFSAALGYRYYGT
TKVCWLSTENNFIWFSFIGPACLIILVNLLAFGVIIYKVPFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYRRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

TGGAACATATCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAATAACATTTACATTAAAGTCATCGAAAGTACAGATAGGTATA
GGAGTCTATGTGCATTTTGAATACTCACCTGATACCATGAATGCGAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCTCTGGTCTCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCTACTGATTTGTCTTGCCATATGCATTTTACCTTC
TGGTCTTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVLR T VAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLR LPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCGGGAAGATGCGCAGGAGGAGCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCAA
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAACTGGGTGCGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAC
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAATATGTGAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG
CCGCGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCTGCGAGTTCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRL
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSPQKSNSSSKATTMSENVQWLTPVIPALWAAAAGSGRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT
CATGCTGCTATTCTCTGCAAAATACCTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGGAATAAGTAACTTCTCTTCTCCAATATGCATGACATTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCACTGGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAACTCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACATATTGCAAAAATTGAATACTCCACAG
ACTTTCAGTAACACTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAAATGTAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
ACTGCTTCAAAAATGTCTGTCCGAAGTGAAGCACTTACAGAAGCTCTATATTAAATCAACAAT
TGCTTTCTACAATTTCACTGGAGCCTTTATTTGGCTACATAAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAGACATGAATTTTAAAGCCTCTTATCA
ATCTTTCGACGCTGGTTTATAGCTGGTATAAACTCAGAGAAATACAGATAACGCCTTGGTT
GGACTGGAAAACTTGAAGAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTTCTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTTAAAGAAAAATGAAGC
TACTAACAAACCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTTCATGGAGCCAGATTCACTGTTTTCGCTGGACC
CACCTGAATTCGAAGTTCAGAATGTTTCGGCAAGTGCAATTCAGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCTCTTCTAATCTAAATGAGAAGCTGGAGCTATGT
TTCTTTCACTGTAGAGCTACTGCAGAACACAGCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTCTTGCTAATACCTGCAGACAAGTTCTATGTCCATTCTGAGGGAACTA
GATATAAATGGCGTAATCCCAAGAAGGGGGTTTATATACTTGATAGCACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATAAAATAAGAGATATTTCAGGCCAATTCAGTTTGGTGTCTCTGGAAAGCA
AGTTCTAAAAATCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATCTCA
TGCTGCGCAAGTGTCTGGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTTGTATTGATATCCACCATCTATCAGAAAAACAGAAAAAA
TGTGTAATGTCAACACCAAGGTTTGCACCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACACACTTATGGCTGTCTTGGAGGCCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCTCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAAATCTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCTCTCTGATATAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACACTCACTGAAAGTAAAGCACTGTTATAGGTTTACCAACAATATGTCTT
AAAAACCACCAAGGAACTACTCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLLQTNNAIKI EYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHLLRLHLNSNRLQMINSKWFDA
LPNLIELMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESI SFYDNRL
IKVPHVALQKVVNLFKFLDLNKNPINRIRRGDFSNMHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTTESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGGQNVVRQVHFRDMMEICLPPIAPESFPSNLNV
EAGSYVSFHCRTAEPOPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGA AACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACTTTAC
CACGCTTGTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTG CAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGC AAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTC AAACTGACTGTCTATGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTAAACAACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWCHDCTLQQVLRSMASNHETAHNVIC KTSVLDEHAGR PFL
NAANDADLCNLPPKTTDYAMLVTMFGWFTMVISYV VYYVRQNQEDARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCAAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGGCATCCCCACCAGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCAGCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGCTGGAGGCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCGAGCAACGCCCTGAAGCTCATC
CCGTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACCAAGAT
CGTTATCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGAGGCGCTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTAACGACTCAAGTCTTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGCTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGTCATGAGCTGCTCCGGCTGACGGAGATCCAGCTGGTGGGC
GGCGAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTGTGTCCA
GGCAAGGACTTCAAGCACTTCCCTGATGTGCTACTGCCAACTACTTCACTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACAGCGTGCACTT
GTGTGCCGGGCCGATGGCGACCCGCCGCCCATCCTCTGGCTCTCACCCGAAAGCACT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACCAACGGCACGTCCTGTGTCATCGCGGCCAACCGGGCGGCAACGAC
TCCATGCCCGCCCACTGTCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCCAACAA
GACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCTTTTCCCTCTCGACATCAAGACCTTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCTCTCTCTGCTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCACATGAAGATGATAAGGCGGGGGCGGGGGGAGGGACCCCGG
GGCGGCCGGGAGGGGAAGGGGCTGGTCGCCACCTGCTCACTTCAGTCTTCCACCTC
CTCCTACCTTCTACACAGCTTCTCTTCTCCTCCCGCTCGTCCCTGCTGCCCCCG
CCAGCCCTCACCACTGCGCTCTTCTACCAGGACCTCAGAAGCCAGACCTGGGGACCCCA
CCTACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACCAACCGCACGCGGAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT
TATGAAACCTTGAATAATAAAAAAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPELLACWQPILLVLVLSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFFNNLFLNRLTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLSNLEQLTLEKCNLTSPTEALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTFNCLYGLNLTSLSITHCNLTAVPYLA VRHLVYLRFLNLSVNPISTIEGSM LHEL
LRLQBIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTITLEESVPHSVGNLETILDSNPLA
CDCRLLWVFRRRWRLNFRNQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDP PPA ILWLSPRKHLVSAKSNGR LTVFPDGTLEVRVYAQVQDNGTYL
CIAANAGGNDMSMPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACC CCCTCCCATCCCCAGCCCCGGGGATTGAGCTCGCCAGCGCCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGAATGGGGGCCCCAGCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTCCGCTGCTGCTGGGCGCCCGGCGGGGCAACCTCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTGAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAACTGTGAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTGACGAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCATCTCTGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCTCCAGCACCTACCAGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGAGGCGCCTGCCCACTTCTGTG
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGACAGGGCCGCCCTCCCGCTTGCTCCCGAGCCACCCACCCCTGTACAGAAATGCTGTG
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGGCGGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC
CAAAATCAAATCTGTCTCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRILQVLTSTPHELSSISISNVALADEGEYTCSTFTMPVVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHLHCEGRGNPVPQYYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCCCTGG
 CTTCCGGACATTGGAGCACATAAATGAACCTTGAATTTGTGCTGTGGCGAGCAGGATGGTCCGCTG
 TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
 GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAGGAGAGA
 TCTGTTCTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGGCTTCACA
 AGTCTGCAGCGCTTTACGCTCCCGACTTCCAGTTTACCATTATTCTGCGATGGCAATTTC
 CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATCCGGTTAGTTTGCACATGG
 AAAACAATGGCTTGCATGAATTCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
 CTGCACATCAACAACAACAAGATCAAGTCTTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
 TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
 ACTTGAACAAGCTGGAGGTCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
 GTGTTCCAGTATGTGCCCATCACCCACTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
 CTATGAGGAGGTCTTGGAGCAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTT
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAACCAATCCCAAGAATGCC
 CTGATCGGCGGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAGAGACCTCAATGAAC
 ACCGAAACGAGACTTGTGTCTTTGAAACCCGAGTGGATTCTAGTCTCCGGGGCGCCCTG
 CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
 GATCATGCCACACAGGGTCTGCTCCAAACGGAGGTACAAAGATCCGAGGCAACTGGCAGAT
 CAAAATCAGACCCACGACGATAGCGACGGGTAGCTCCAGGAAACAAACCTTAGCTAACAC
 GTTTACCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTCCGGTTTAAAGATGAAC
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTGAAGCCCCAAGCTCTCTAACGTGCAGGA
 GCTTTTCTACGAGATAA CAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
 ACCTCATCTCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAACCTGGACACGCTGCTCCGGGA
 GAAATTGCGGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
 TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATCTCAACAACAACCTG
 CTGAGGTCCCTGCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGGACAA
 CAATTACTTCTATGTAACCTCCCGGTGGCAGGGGTGCTGGACCACTTAACCTCCATCATCCAGA
 TAGACCTTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCTTTCAAGCAGTGGGCA
 GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
 TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
 CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC
 AACTCTTACCTAGACACCAGCAGGGGTGCTCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
 GTTTGTCACTCCGCTTACCGTGGTGGGATGCTCGTGTATTCTCTGAGGAACCGAAAGC
 GGTCCAAAGAGACGAGATGCAACTCCTCCGCGTCGAGATTAACTCCCTACAGACAGTCTGT
 GACTCTTCTACTGCGACCAATGGGCCTTACAACGCAAGTGGGGCCACAGAGTGTATGACTGT
 TGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGCGC
 ATACATCCTTCCCAACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCGCG
 CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCAACAACCGAAAGGGCCT
 GACCCCTTACTTACTGCTCCTCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
 GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCAGCAGACCTGCTGGAAG
 AACTGACAGTGCCTCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCCGGGTTCTATAC
 ATATATACATATATCCACATCTATATAGAGATAGATATCTATTTTCCCTGTGGATTAG
 CCCCCTGATGGCTCCTGTTGGCTACGACAGGATGGGCAGTTGCACGAAGGCATGAATGTAT
 TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLETS LCFAAGNVTDGVCCEKICSCNEIEGDLHVDCEKKGFTSLQRF TAPT SQFYH
LFLHGNLSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKNKISFRKQ
TFLGLDDLEYLQADFNLLRIDPGAQFDLNKLEVLILNDNLISLTPANVFQYVPITHLDRG
NRLKTLPEVEEVLQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVSSSLPAPPAQEETFAPGFLPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPGGCSCDHIPGSLKMNCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLRSREKFAGLQNLEYLVNEYNAIQILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPPKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEITCPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVVISVL
VPGLLLVFVTS AFTVVGMLVFILNRKRKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAACTGTTGGC
CGCTGGGCCCGCGGGGGATTTCTGGCAGTTGGGGGTCGTGCGGAGCGAGGGCGAGGGG
AAGGGAGGGGAACCGGTTGGGGAAGCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGCTCAG
AGAATGAGGCGCGGCTTCGCCCTGTGCCCTCTTGGCAGGCGCTTGGCAGCGGGCGGGCGG
CGCGGAACACCCACTGCGGACCGTGTGCGTGTCTGCGCCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATTGAAGCGGCAGGCGGCCGAGGAGGCCCTGCATCTCGCAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTGCGCTCTGCGGGCAGGCCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCTGGCTGTCCTCCGACCCCGCGGCTC
GAAAGCGACACGCTGCGAGTGGGTGGAGGAGCCCCAACGCTCTGACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCGCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCTCTGCC
GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAACTGCCTAGACACTTGGGAGG
CTTTGCGTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACACAGGCGCCCGCGGCCACT
GCAACCGCCCGTGCCGAGAGAACATGGCCAATCAGGTCGACGAGAAGCTGGGAGGAC
ACCCTTGTCTCTGAACAAGACAATTGAGTAACATCTATTCTTGAGATTTCTCGATGGGGAT
CACAGAGCAGATGTCTACCTTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCTCAGGCTTT
CGACTCCTCTCTGCGGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGCTAAGCTCTGCTTTACGAAAGCCCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACATGGGGTGAAAGTCGGGGACTGTGATCTGCGGACAGAG
CAGAGGGTGCTTGTGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTAC
TTGTGTAACGACAAATTTTGCAGAAATCCCCCTTCTCTAAATTTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTAGGA
TGGTGATCTGGGGACCGGCTAGTGCTGGGGAGAGATATTTTCTATGTTTATTTCGAGAA
TTTGAGAGAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA
TTAAAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTGTTTTCAGGCTAGGAGTAT
ATTGGTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEFACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQORSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCDDDLGGFACECATGFE LGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSFPVQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQA F DSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPPSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTGAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCCGCTATC
CCCCGGCTACCTGGGCCGCCCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGSCAGCCGA
GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGCGGTGTGTGCCCGCGCGCGCGCGCTGGGGTGCAAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAAGCCTGGGCGCCACTCTGCCTGCTGTGCTGCGGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGTTTTCTCTGGAGTGTACCCTCCAAATAGCAAAATGTACTTTGGAAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAAATGGCCATGCCAATGGCCAGCGCATTTGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAGATTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGTGATAGTCCACCCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTTCAGGCCAAAA
AAACTGCCATACAACTACAGAACAGCCTGTCAACACCACATTCCCTGTAAACCAGGGTTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CAGGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGGGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGCGAGGCAAAATCATGCCCCAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAAAGTGAAGTGTGCCATTTAAGCTGTATTCTGCCATTGCGCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTTCATGATGAGGATGAGGCCTCCGAGATAGCTGAGGGGAAGTTCTT
TGCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCGCATCTAGTGCAGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGGAAGCGTTTTATTATACATCTCTGTAAAAGGAT
ATTTTGAATTTGAGTTGTGTGAAGATGTCAAAAAAGATTTTGAAGTGCATATTTATAGT
GTTATTGTTTTACGCTTCAAGCCTTTGCCCTGAGGTGTTACAACTTGTCTGCTTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFVTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAEPNERGDQYCGLLDRPSGSFKTFNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSENNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGGCTGGGCGGTGCGTTCCTT
CCTTCTCCGTGGCCACGAGGGTCCCCAGCCTGGGTAAGATGGCCCCGGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGTTTGACAGCTTTAACAAGGGCTTGGAGAGAACCTCCGGGACAACCTTGGAG
GTGGAACAACATGCGCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCTGTCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCTGTC
CTTCCCTGTCTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
CACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACCCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGACAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCACCGCTGCCCCAGAGCTTGGGCTGCCC
TCCTGTCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACATGTGTGA
ATTTCAAAGTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCAACCATCCCCACACCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGAAAGTTAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSERLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGGQCEGEGTRGSGHCDQCAG
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPBESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTDELVVLLQQMFPG
IIICALATLAAKGDLVFTAFIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCCTCTGGGTGTTGCCCTTGGCCAGCCCCGGG
GCCGCCCTGACCGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCTTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGTGTCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTGGCCCGCAGGTTCTTGGCGTTGGAGGCCAGCACACCTGTGTGTGTTTCGG
CATGGAGCAGCGGTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGTGTCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCTGTCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCCGTGGCGTCCGGCGCCACAAAGCTGGTCCGCTTTGCCCTGCGAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGCTCCAGCCATAGCGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAACTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCATATATTCTAAGCACTTACAT
TGGAGATACTGTAACTTGGGGCAGAAAGCCANTGTGTGTCATTGTTTACTTGTCTGTGTCAC
TGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFPQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLG DYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLEPNMRVQKCSCASD GALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGTCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATATGGTCTCTGAGGAAGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCCACCATTGGGAACCGGG
CAGTGTCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCATACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCTATGTCTCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTTCATCGTGGCAGCGCTCCTTGTAACCTGATTTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGACTCTGGCCCCCTGATGTCTGTAGTTTTACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTCTCTACCACTGCTGAGTGGCTGGAACTTGTTTAAA
GTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATTGGGAAGTG
CCACTGGGATCCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCAGAGGCTGAGGACAGGCGGATCACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAAACCTACTGGAATAACAAGTTAGCCAGGCATGGTGGTGATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGDTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEBEGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGC**ATG**AGCGGCGGTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGCGAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCAGTGGCGACCAAGTGGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCCTGCCCTGCAACCGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTGACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCGACTCCAGCGACGAGCTCGGCTGTGGAAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCCTC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGAGACCACTCTGGAAGCCCACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCCTTTGTCTTGCTCCGAGCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCC**TGA**GGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
GGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSSGSCPPTKQCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPTQKGQCPPPPGLPCPTGVSDCSGGTDKKL
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTS LRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTACGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCGATTTCAGTCCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTTAATGGAACCTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCGCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGTGCTTTCCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
CCTTGCTCTGGAAGCCCCAAGTCTGTCCACTACCTCCAATGGTGAGTACAGGAGATTTCTGTCT
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAACGTGGTGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAACGTGGCCAGCACCCATGAGACCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTTGTGTGGTAGACGGCGTGCCCGTCATGTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAAGAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAACCTTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACAGCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGCTCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCTCTTCTCTCTGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGCTGGAAGCTTGATCAAGTC
CTGTTTCTCTTGACACAGACTGATTAAAAATTTAAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDABIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATATSVLLVLLLVILARMFQTKFAHFPPRGPSPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCC**ATG**AGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTGTGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATT'TAC'TTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCAATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAAATTTAGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCAATTTGCAAAATATTCTGATGAGAAACAGCAGTTCCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCTTCTCCTCCTCCTTGTGCTACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGAAAATGAAATATATG
GTTATT**AGG**ACATATAAAAAACTGAAACTGACAACAATGAAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACAAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAAACCACCTCTGTTTTCTTCTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAAATCAGAATCTTTCAAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI~~ES~~ED~~EQ~~KLIEKF~~IE~~NLLPSD~~GD~~FWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRN~~WY~~VDEPSCGSEVCVVMYHQPSAPAGIGGPFYMQWNDDRCNMKN~~NF~~ICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPL~~LL~~LV
VTTVVCWVWIKRKRKREQDPSTKKQHTIWPSPHQGN~~SP~~DL~~EV~~YNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSES~~SG~~FVTLVSVESG~~FV~~TNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGACTTGGGGCGCCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCTCTCTGCAGCCTCAACCCGAGGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGAACCCCGAGCTATTAGAGGTCCCAACCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCCACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGTGAAAGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAAATAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAEIQEADGQCPVDRSLLKLKMVQVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQMQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLPSCPMLKRFRMIEQRAVDTSLYILPKEDRESLQMAVGPFPHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPDMLNAMSYYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTTGCACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAAACCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGTGTGAGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TATGGCCGGAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAAGCAACCCCTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCACGACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCAGGCCTCCATAAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACAT
CACCATTGTCTCTGTTTCTGGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGGATAAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATCTGGTAACCTTATTACAAATAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGGLHRCCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESFSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTTVCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPGWKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCCDNWGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACACGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGCTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTTGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAAACAGTAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGMISI
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAATTTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGCGCAAAATCGTCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTCTCTGCAATGACGAAGAATAACCATGGCCATATTTGCTACTGTGGCTTCGGCAG
CTGGACATGTCTCGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAAATCAGTGTAAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATTAAGCAGCTAGTTTTCTGAAAACGATTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCAGAAATTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCATTCTTCAATA
TCATTTTGGAGCTTTGGCAGTCTTCATTTACTACCCTTGTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTGATTGCACTTAAATTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACAGTGTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIIVTVASAAGHVSVFPLLAYC
SSKFAAVGFGFKTLTDELAALQITGVKTTCLCFNFVNTGFIKNPSTSLGPTLEPEEVVNRMLH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAVIGYKMKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAGAGAATTGAGTTTGGTCGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCAGCTCAGATACAGCCAGAAGATGCCCAAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTCTACCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTACAAAGTAACATGA
CCTTGGCTGACAGAGACTTCCCTGGACCAACCGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCCTAATTCAAGTTTTCAGATAITTTCTGAAATATAAAAAATA
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGGCTTTGAGCCTTTGAAATACTGGATAAACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATATAGTTGAAAAGTACTTGCAGAGA
AGATACAGTACAGTCAAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCAATTTATGAAAAAGGATGGGATCCTTATGTTGGATAACTACCTTCCCAAAGAGAACAT
CAGAGGTTTTCAATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCTAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTCATCAATAAAATATCCTTGAAACCAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAAGATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAAGTGAAGGTGACAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAATATATTGGATAAGAAATAGCTCAATTATCCCAATAAAATGGATGAAGCTATAA
TAGTTTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAAATCTTTGAAATA
AAAAATATTATATATAAAGTAAAAAATAA

CGGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCTC

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLTVNKTYNSNLFWFPPAQIQPEDAPVVWLWQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLSNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKQYFQKQCHECI EHIRKQNWFEAFEILDKLDDGLTSDPSYFQNVGTG
CSNYYNFLRCTPEPEQQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIIYNGQLDII VAAALTERS LMGMDWKSGSEYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
 TTTTCCCTTTCTCAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
 GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCCTGCTTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCCGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAAATGACTGGCTGGG
 TGAACCTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
 TAGAGATCTCTTTGTAAAATAAAATTTTAAAAAAGCAAGTAATTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCTCTGAACATTCCTTAAGAGGGAGAAAGTATGTTAAAAATA
 GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACAGGATGGGGACCTTGGGTC
 AGGCCAGCCTCTTTGCTCTCCCGAAATTATTTTTGGTCTGACCACCTCTGCCTTGTGTTTT
 GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGCTCT
 CCTCACCGCCGCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
 ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
 CCACCAAGGGACGGGGCCGCTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
 ACCTGACCATCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
 CCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCTTCAACAACATGTCAACAAGCTGCT
 CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGGAGCCTCTACCAGGGGCTGTGCA
 AGCTGCTGCGGCTGGATGACCTCTTCACTCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
 CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
 TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATACTTCCCGACCTGTCCA
 GCCGAAGCTGCCCGGACCCCTGAGTCTCAGCCATGCTCGACTGAGCTACACAGCAT
 TTTGTCTCTCTCTCATCAAGATCCCTTCAGACACCTGGCCCTGGTCTCCCACTTTGACAT
 CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
 CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACTCTTCTACACCTCACGCATCGTGGG
 CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGCTCCTGCCCCTTGGGCTGCACCCGGG
 CGGGGTGGAATACCGCCTCTGCAAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCTTCAATATCACAGCCAGGACGATGTACTTTTGGCATCTTCTCAAGAGGCAGAAAG
 CAGTATCACACCCTCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT
 GCAGATCAAGGAGCGCTGTCAGTCTGCTACCAAGGCGAGGGCACTTGGAGCTCACTGGC
 TGCTGGGAAGGACGTCAGTGACGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
 CTGGACATCAACCAGCCCTTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
 CAGCAGGAGCCGATGACCTCTGTGGCTCTTACGTTTACAACGGCTGACAGCGTGGTTTTTG
 TGGGAGCTAAGAGTGGAAGCTGAAAAAGGTAAAGTCTATGAGTTAGATGCTCCAATGCC
 ATTCACTCTCAGCAAGAGTCCCTCTTGAAGGTAGCTATTGGTGAGATTAACTATAG
 GCAACTTTATTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAAGAGGGTTAAATTTTGTG
 ACTTAGCTTCTAGCTACTTCTCCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
 TTTCAATATTTCCCAACTTTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLGQASLFAPPNGNYFWSHSAALCFASCEGQPGKVEQMSTHRSRLTLTAAPLSMEQRQFPW
RALEVDSSRSVLLSVVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLRPRDPESAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFGGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFALFSGKQKYHHPDDSAALCAFPPIRAINLQIKERLQSCYQGEN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVVFGTKSGKLLKKVRVYEFRCNSNAIHLLESKESSLEGSYWWRFNRYQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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AGGCTCCCGCGCGCGGCTCTGTGGCAGCTCGAGTGGGAAACCCGGTCCCCGCGCTAGAGAAACAGCGCATGATGACCA
 CTGGAGCTCTCCGCGGAGCGGCCGACCGCCAGCTGGGAGCTCTGTGCTGTGTTGGGCTTCTGGGCTCTCTGGTCTCC
 GCAGGCTGACTGAGACCCCTGGTCCCTCTCGGGCTCCGCACTGACAGCTGGGGCTGCAAGCAGCAAGGCTGGA
 ACTTCATGCTGGAGGATTCACCTCTTGATCTTCGGGGGCTCCATCACAATTTTCGTTGGCCACGGAGTACT
 GAGGGAGCCGCTCTGAGATGAGAGGCTTGGGCTTGAAACACCTTCAACCACTTATGTTCCGTGGAACTGCATG
 AGCCAGAAAGAGGCAATTTGACTTCTCTGGAACTTGAACCTGGAGCGGCTCGTCTCATGTGGCGCAGAGATCG
 GGCTTGGGTGATTCTTGCCTCGAGGCCCTTACATCTGACGTGAGTGGACTCGGGGGCTGCCAGCTGGCTACT
 TCCAAAGCACTGGATGAGGCTGAGGACCACTTACAAGGGCTTCAACGAAGCAGTGAACTTTATTTTGACCACTG
 TGATGTCCAGGTTGGTCACTCAGTACAAGCTGGGGGACCTATCTTCCGTGTCAGGTGGAGAAATGAATATG
 GTTCTTATTAATAAGAGCCCGCATACATGCCCTCGCTCAAGAAGGACCTGGAGGACCTGGCATTTGGAACTGCT
 TGCTGACTTCAACAAGCAAGAGTGGGCTGAGCAAGGGGATCTGCAGGAGTCTTGCCACATCAACTGCACT
 CAACAACAGAGCTGCAGCTATGCAACCTTTCTTTCAAGCTGACGGGACCTGACGCCAAGATGGTGAATGAGT
 ATGGAAGCGGGTGGTTTGACTCGTGGGAGGGCCCTCACAATTTCTGAGTTCTTGAGTTTGTAAACACCGTGT
 CTGCCATTTGGGACCGCGCTCTCCATCAACTCTACATAGTCTCCAGCGAGGACCAACTTGGCTTCAATGAT
 GAGCATGCACTCCATGACTACAAGTCAAGATGACAGCATGACAGCATGACTATGATGCTGTCTGCAAGAAGCCGCG
 ATTACACGGCAAGTACATGAAGTCTTGAGACTTCTTGGCTTCACTCAGCATCTCTCCCTCCCCACCTG
 ACCTCTTCTCCAAGTCGCGTATGACCTTTAAAGCCCTTAAAGCCGCTTGTACTCTGTTGGGACGGCTCAAGTAC
 TGGGGAGCCCAATCAAGTCTGAAGAAAGCCATCAACATGAGGAGCACTGCAGTCAATGGGGAAATGGACATCTCT
 TCGGATCACTTCTTATGACACCAATCACTCTCTGTGGACCTCTCACTGGCCACGTGACTATGTCGGGGGACG
 TGTTTGTGAACAACGATATCAATGAGTTCTTGACATCAACAACGAAGATTCGTCTCCCTCTGATCCAGGTT
 ACACCGTCTGAGGATCTTGGTGGAAATCTGGGGCACTCAACTGGGAGAAATATGATGACAGCGCAAA
 GCTTAAATGGAATACTCTATCTGAATGATTCAGGCTGAAAACCTTCAAGATCTATAGCTTGATATGAAGAAG
 GTTTTCTTCAGAGTCTCGGCTGACAAATCCNCTTCCCTCCAGAAACACCACTACTCTCTTTCTCTTGCG
 GTAGCTTGTCCATCAGCTCCAGGCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAGGGGGTTGATTCA
 TCAATGGCCAGCACTCTGAGCTGTACTGGAATCAATGGACCCGAGAGAGCGCTTTACTCTCCAGGCTCCCTGGTTGA
 GCGCGGAATCAACAGGCTCATGTTTGTGAGGACAGATGGCGGCTCTGCATACAGTTACGGAACCGCCAC
 ACTCGGCGAGGACCAAGCATATTAAGTGAACGCGTGGCCACCCCTCTCTGCTGTGCGAGTGGAGAGCTGCGCCCT
 CTCTTGAGCTGGAAGCTGTGGTGCTGCTGCCCAACCTTCTGCAAAAGAGCTCTTAAGTAGTCAACCTCAGGAG
 ATGCGGGGCTACAGTCTGCCCTCTGTCTACAGCTCAAAACCTTAAGCTCTGAGGAAAGGTGGGATGGCTCTGGCC
 TGCTTTTGTGATGAGTGGCTTTCTCAACGCTGCTCTTGTGCGAGGCTGTCCGGCTCTCTTGAAGTGGAGCG
 AGCTAAATCAGATCCGCGACCTTTGGCCCTCAGAAAGAGTGTGAAACCTGCCCTTGACCGAGAGCTGACACCC
 TCGAGACTCTGCTGAGCTCAGCGCTGCTTTTGTGCTGTCTGGGAGGCTGTGCCACTCCCTATGGCCCACT
 TTTATCCCCGAAATCTGGGTGTGTCACAGCTGAGAGGCTGGGAGAGGGGTGCTCTACCTGAGTGACTTTGTT
 TCTCTTCAACAACCTCTGAGCTTCTTTGGGATTTGGAAGAACTCGGCTGAGAAATGTGACTTCCCTT
 TCCCTTCCCACTCGTGTCTTCCCAAGGGTGAAGGCTGGGCTGGGAGAAACAGAAATCTTCCACTCTGGCTCTCC
 CAAGTTGACAGGTTGCTCTGTGTTGTCACTGAGGAGGAATCACTGAGTCTGTGCAAGGACATGGCCGATCTGCA
 CATCAGGAGGAGGAGCAAGAAGGCCAGCTCAGATCAGTGTGAGTCTTGCGAAGGACATGGCCCATCTGTGCATCC
 AGGGAGGAGGACAGAGGCCAGCTCACTGATGTGAGTCTGCGAAGAGCATGGCCCATGTGTGCATCATAGGGA
 GAGGACAGAAAGCCGACTCAGATGTGATCTGTGCGAAGGACATGGCCCATGTGTGCATCATCAGGAGGAGG
 ACAGAGAGGCCAGCTCAGTGGCCCGCGTCCCAACCCCAACCGCGAAGCAGAGGGGACAGACGCCCTCTCT
 GAAGTGTGCTCAAGTCCGATTTGAGCTTCTTGTGGGGCCGACCCCAACCTGGCTTGGGCTCACTGTCTGA
 GTTGTGAGTAAAGCTATAACCTTGAATCAAA

FIGURE 64

MTTWSLRRRPARTLGLLLLVLVGLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPFWLLQDPGMRLRTTYKGFTAEVDLYFDHLSRVVPLQ
YKRGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFDSWGPFHNILDSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSI SGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTVSI GF LDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVV FINGQNLGRYWNIGPQKTL YLP GPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCAGGACC
 CTGTTGAGGGTTCTCTACTTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAACACGCCATGGCTCCC
 AAGAAGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
 GGCAGACACTCGGTCTGTTAGTGGATAGGGGTCAAGCCGGTTTCTCTAGACGGGGCCC
 CGTTCCGCTATGTCTGCGAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACGAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTCCGTGCACCTGTAGG
 AGAAAGAGCTTTGCTCTTACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATACCCTGTAGATTTTGGCCGAGCTGACAACTGACCAAATCTTTACCTTGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGCTGAGCTGTAAACCAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
 AATGGTCCGATAAGAAGGGACGCTTCCTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTTTCGAGATGTCTATGACCAAGT
 TCCAGGAAGTTCTCTTTGGGACCTTACCTCCCCCGAGGCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCTAGACTTGCTTTGCCCCCGTGGGCCCAT
 TCATTCAACTTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTGTAGCCAAACACCATTTCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCCAGGGTGTGTGGAGCGAAATATGAG
 AGACAAACTATTTTTCACGGGGAACCTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAACAACCTCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTTGGAAGTG
 GTGGTTTCCCCCTCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAGTCTGGATCAATGGGTTAACTTGGGCCGGTACTGGCAAAAGCAGGGGGCC
 ACAACAGACCCCTCTACGTGCCAAGATTCCTGTGTTTCTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
 CTCATATGACACTAGTACTTTTGACAGGACACATATCAATTCCTTTACGCTGATACACTGAG
 TGCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGTTGGCTCATGC
 CTGTAATCCCGACACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTACGAGCTTCAAGA
 CCAGCCTGGCCAAACATGGTGAACCCCGCTCTCCACTAAAAATACAAAATTAGCCGGGCGTG
 ATGGTGGGCACCTCTAATCCCGACTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGTCAGTGAAGTGAGGTTGTACCAGTCACTCCAGGCGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLPLSLTLLLPQADTRSFVVDGRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPBGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEFGHPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM YMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILEPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVFN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGLKLSKLDILVENMGRLSFGSNS SDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGD TFLYL
PGWTKGQVWINGFNLGRYWT KQGPQQTLYVPRLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEFMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGCTCTGCAAGCCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTCAGTACATTCCAGATGTCAAAACGATTTT
GCGTTCCTTCTTACATGGTAGACCAGTATGACCAGCTATATTTCCAAGCGTTTGGTGTGTT
CTTGTCAAGATTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTCGGGGGTGCCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAAGCTAAAAATCCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCCTCACGTTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCAGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTTCGCACAATTCAGGAAATCATCAGTTTCCAGCATTTAAAAAGACT
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAAGTGCATCACC
TCACTCCAGAGAAAGTTGGTCACTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACCTG
CTTGACCCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTGTG
TGGAAGATCACCTTTTGTATACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTCTTGCAAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTAAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGTTTAAAGTCATTCAATTTCCAAATCATTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATATATAATCACTAATCTTGGTTCTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATGACATT
TTCTTACTAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFIGLYTLFWLFRIPPLKEYSFEKVRRESSFS DIPDKNDFAFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTTFEKL RQHISRNAQDKQELHLFMLS G
VPDAVFDLTDLDV LKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNS ENNKMIGLESRLRLHLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAE LELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRLCDVSYNNISMIP IETIGLLQNLQHLHITGNKVDILPKQLFKC IKLRTLNLGQNCITSLP
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDHLFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCGGACTTTGCATTTCATTCCCTTTTCATTGACAACTGACTTTTTCATTCTT
 TTTTTCCTCCTCTGGGCCAGCTTTGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTACACACATAGGAT
 CTGTGTTTGGGGTTTCTTCTCTCCCTGCACATTGGCATTGCTTTAGTGGTGTGTGGGGAGGGAGACACAGTGG
 GCTCAGTGTCTTGTCTGCATTATCTGCCTAGGTACATCGAAGTCTTTGACCTCATACAGTGATTATGCTGCTC
 ATCGCTGGTGGTATCCTGGGGCCCTTGTCTCTGCTGATAGTTGTGCTGCTCTGTCTTTACTTCAAATACACAAAC
 GCGCTAAAGACTGCAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCCAGACAAAGGTGTGGTGGGCGAAG
 AACAGCCAGGCCAAACCATTTGCCACGGAAGTCTTGTCTCGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
 AGTTTTGATTCCCTGCCACTTGTCTGTTGGGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACTGTTTGTGATGTGCGAGCACAGAAGAAAGGCACAG
 CTCCCATCAGTTTTCATGGAAAAATACTCAGTGTCTGTGGGAACCAAGCTGTGTGAGGATCCCTACAGAGAGCTTC
 CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGAAATGCTGATAAACCAAGTCA
 CACAGCTGCTCTATTCTCACACAAATCTACCCTTGCCTGGCTGGAAGTACGCTTCCCTGGAGGTGTCCAGAAA
 GCTGATGTAAACACAGAGCCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGCGCCTTGCCAAATGGAGCTTGTGA
 AGAAGGCTCATGCCATTGACCCCTTAAATCTCTCTCTTGTGGCGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCACTAGGGGGTGCATATATGGCAGAGACCCACAAGCCATGATCCTGCAACTCAATCCC
 AGTGAGAACTGCACCTGGACAATAGAAAGACACAGAAAACAAAGCATCAGAATTATCTTTCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAGTGAACCATTAAGTCTTTGACGGAACTCCAGCAATGGGCTCTGCTAGGG
 CAAGTCTGCAGTAAAAACGACTATGTCTCTTATTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
 GACTCAGCAAGAAATCAAAGAACTGTCTTGTCTTCTACTCTTCTCTCTCTTAAATCTCTATTCCAAACTGT
 GCGCGTTACCTGGATACCTTGAAGGATCCTTCCACAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
 TGTGTGTGGCACAATCAAGTGGAGAAAGATTACAAGATAAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC
 AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGACAAAGTCTGT
 GCGCGTGTGACTCCCACTTCGAATCGTCATCAAACTCTCTGACTGTGCTGTTGCTACAGATTATGCCAATTCT
 TACCGGGGATTTCTGCTTCTACACCTCAATTTATGAGAAACATCAACACTACATCTTTAACTTGCTCTTCT
 GACAGGATGAGAGTATATTAAGCAAACTCACTAGAGGCTTTAACTCATAGGGAATACTTGCAGATAAA
 GACCCACTTGCAGACAAAATATCAATGTGTGGAATTTCTGCTCTCTTAATGGATGTGGATCAATCAGA
 AAGGTAGAAGTCACTCAATATCTTACCAATATCACTTTCTGCACTCTCAACTTCTGAAGTGATCACC
 COTCAGAAACAACTCCAGATTATTGTGAAGTGTGAATGGGACATAATTCTACAGTGGAGATATATACATAACA
 GAAGTGTATGAATCAAAAGTCAAAATGCACCTGGGCAATATAACACAGCATGGCTCTTTTGAATCCAATTCA
 TTTGAAAGACTATACCTTGAATCACCATAATTATGGGATTGAAACAACTCTTTTGTCTCAAGTTAGTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTCTTCTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCTCTTCCAACT
 TACGACCTAATCAAGAGTGGATGTAGTGCAGATGAAACTGTGAAGGTGATACCTTATTTGGACACTATGGGAGA
 TTCCAGTTTAAATGCTTTAAATCTTGTGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATATGTGAT
 AGCAGTGACCACAGCTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAACGAGACATTTCTCATATAAATGG
 AAAACAGATTCCATCATAGGACCAATTCGTCTGAAAAGGATCGAAGTGCAGTGGCAATTCAGGATTTCAAGT
 GAAACACATCGGGAAGAACTCCAAACAGCCTTTCAACAGTGTGCATCTGTTTCTTCTATGGTTCTAGCTCTG
 AATGTGGTGAATGATAGCGACAATCAGATGAGGCATTTTGAATCAACGGGCAGACTACAAATACCAAGAGCTG
 CAGAATATTAATCAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAATGCTACCTCGT
 GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAGTGACACACAGGCCCTGCATGTAAAAAAA

FIGURE 70

MELVRRMLPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDDPGSCSENIKVFDGTSSNGPLLGGVCSKNDYVPVFESSSSSLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSTSPNYPKFHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKDFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIIFSASSTSEVITRQKQLQIIVKCEMGNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKITLESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGCG
TGCTGCCGCCGCGCCGTGCCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
CTGGAACGCCCGCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTCCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAATGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGGACTGTACTATTCCCTTTTTGA
ATGTTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCGATTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAATGTCATGACAATAGACAAACTGCTCTGGGGCTATAGGAGGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTATGAAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTTTGGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCAGAATGACACTGTCAACCCAGATGTGTGTGATACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTCTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTAATTGGCAGTTCAGCCCTTTCCCTTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCATTTGGCATTAAAGTC
TCTTCACATTGATTGTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGTTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTTATAAAAAAAA
GTTTTCTTTCTTCAATTATAAATAACATAAGTGTACTGTAACTTTACAAACGTTTTAATT
TTTAAACCTTTTGGCTCTTTTGTAAATAACCTTAGCTTAAACATAAACTCATTGTGCAAT
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQFEVLWSDGGGAPDQYWNSTGFLAWLY
NESFPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGBEAIYETYT
WRSQNDTVTPDVWYTSKPKKLVYAIPLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCATCCAGGTGTCTGTCAGAATTATGGGGATCACCTTTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCTATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCA
AACTGCAACACAAAACACAGAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTTGTGTACAGAAGTTTATGGAAGTACAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGTGTCTCCTCTCTTCTTTGGTGTCTGCAGCTGGTCTGGATTTTGC
TATGTCAAAGGTAATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGAGAAGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAAGATCCAAGAGTCCAAGCAAACTACCGTGCAGTGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGAATATGGAGTGACCAAAAGAGAATGC
CCTTCTCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA
GGACCTAAAAACTCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGTGTCTGAGGTAGG
TGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCAGCTCAGAC
CCTTCTCTCAGCTCTGAAAGAGAAAAACGATATCCCACTGACATGTCTTCTGAGCCCGTA
AGAGCAAAAGATGCGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACCT
GTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAACTCTTATAAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAAATTC
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATCTCTCAAAAAATGACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA
GTTTTGATATTTCTGATCTTATCTACTTCCAACTAATTTTATTTTTGTCTGAGACTAAATCTT
ATTCAATTTCTCTAATATGGCAACCATTATAACCTTAATTTATTTAATACATACTAAGAG
TACATTTTACTCTTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTTCCAACAAAGGAGCTGAGAGATGCAGAAATATTGTGACAAAAAATTA
AGCATTAGAAAACTT

CGGCTGAGCTGATG

FIGURE 74

MARCFSLVLLLLTSIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLWKVPVSRQF
AAYCYNSSDTWINSCEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETETFFVENKAAFKNAAAGFGGVPTALLVLALLFF
GAAAGLGFICYVKRYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGGGTCTTGGCACCTCTAATTGCTCTCGTGTATTGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCGTGAGGAA
ACTGCGCGCGCTCTGCCACGGTCTGCCCACCCAAACGGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGTATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTGCGATGGGCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATAACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCAGTGTGAGA
TGGGGAACAAGAAGGATAAA TAAGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTCTTCCATAACCAAGCCTGAGGCTGCAGCCTTNNATTNATGTTTCCCTTTGG
CTGNGACTGGNTGGGCGAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTGAG
GCACCTACAGGAAGGCCTGCCATGCTGTGGCCAACGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAAATTTTCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAGATATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCAACAAG
TTTTTATCATTAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGCCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC
TAACCCCTTGACATACTCCCAACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYPNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 78

MGLLLLVPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCTGGGACACGTACGACACGGACCGCGACGGCGGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGCGGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACACAGCCC
CTGTTGGAAGCCAAACCCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCCAGATGAGCTGTGAGCAACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCAGGCATCCTCCTGCCCCTGGGCTCTCAGGGAACCCCTGGGTCGGCTTC
TGTCCCTGTCAACCCCAACCCAGGGAGGGGCTGTATAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCAGACCCAGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGCAATAA
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQKGKSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRGVRVGWEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD SMATRE
ELTAFLHPPEEFHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQ
FRDFRDLNKDGHLDGSEVGVHVVLPAPQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

GGGGCTTGTCCCTTCCCACTCGGGGCGCAGCCGGGTGGATCTCGAGCAGAGTGCGGAGCCCCGG
GCGGCGGGCGGGGTCGAGAGGGATCCCTGAGCCTCTGTCCCTGTTTCTTGTGCGTCCCGAG
CTCTGTCTGTGCTGCTTTTGGCGCCCCGCCCTCCCGCGGTGCGGGGTTGACACCGATCTCTG
GGCTTCGCTCGCATTTGCGCGGAGGCGCTCCAGACCTAGAGGGCGGCTGGCCTGGGACGAC
CGGGTCTGTCTGTGCTCTCTCTCTCTGTGCGCCGGCGCGGGGATCCGAAGAGTGTGCGGGCTCT
GAGGAGGTGACGCGCGGGGCCCTCCGCAACCTTGGCCTTGGCCGATCTTCTCCCTCTCTCCAG
GTGTGAGCAGCCTTACGTACCAATGTCTCGAGCAGCTGGATTCGCGGCTCTCGGCCTCGGTGTG
TGCTGTGCTGTCTGCGGGGGCGGGGACGAGGAGGCGCTCCCATGTGTCTACATGAT
TTTTACCAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTGCC
CTCTTGAGGAATTTCTGTGTATGGGAACAATGATATGCTTCTGTATCGAGCATATGTGGG
GCTGTCTCTCCAGAGGGAGTAATCAGCAACTCAGGGGGACCTGTACAGTCTATAGCTCAT
TGGTTCAGGAAAACCTATTCTCATGATGATGCCAATGCCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTCTTTCCACAGTAACCTAAGGCAAAAGTAGTACAGAGGGCGCCAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAAGATGTAAAGCAGACATTCATTTCTGATTGATGGAAGCTTAAATTTGGCGAGC
CGCGATTTAAATTTTACAGAAGAAATTTGTGTGAAAAAGTGCTCTAATGTGTGGAATTTGAAACA
GAAGGACACAGTGTGGGCCTTGTTCAGGCGAGTGAACATCCCAAAATGAATTTTACTTGA
AAACTTTACATCAGCCAAAGATGTTTGTTTGCCATAAAGGAAGTAGGTTTTCACAGGGGGTA
ATTCCAATCAGGAAAAGCCTTGAAGCATACTGCTCAGAAAATTCTTCACGGTAGATGCTGG
GTAGAAAAGGAGTCCCCAAAGTGTGGTGGTATTTATGTGTTTGGCCTTCTGATGACAT
CGAAGAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGTTCCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACCACATGCCCAGTCTGGTTGGCCACAATAACGTAAA
GCCCTGTGTGACAGAAGCTGTGCATCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCTTTCTCAATTTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCGCTC
ATGCTGTAATTTGGTTTCCAACATGCCAAGACTTTGAAATCTCGGCATGTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTTCAGTTTCACTGACTATAGCAC
AAGAGCATGTCTAGCTGTCTATCAGAAACATCCGCTATATAGTGGTGGAACAGTACTGGT
GATGCCATTTCTCTTCACTGTTAGAAATGTGTTTGGCCCTATAGGGAGAGGCCCAACAGAA
CTTCTCTAGTAATTTGTACAGATGGGCGAGTCTATGATGATGTCCAAAGGCCCTCGAGCTGTG
CACATGATGACGAAGTACATCTCTCTCTGTGGTGGTGTGGGCACTCTGGAATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCAGCCTTTCTTCAAGAGAGTTTACAGGATT
AGAACCAATTTGTTTCTGATGTCTCAGAGGACTTGTAGAGATTTCTTAGAATCCGAGCAAT
AATGGTAACATTTTGAACAATGAAAGAAAAGTACAGAGGGATCCAGTGTGTAATTTGATTT
CTCAATAATCTGAAATGCTTTAGCATACTAGAATCAGATACAAAACATTTAAGTATGTCAAC
AGCCATTTAGGCCAATAAGCACTCTTTAAAGTCAGCTGCCTCTGGTTACAAATTTACAGTGT
ACTTTGTTTAAAAACACTGCTGAGGCTTCAATATCATGGCTCTTGAAGAACTCAGGAAGAGGA
GATAATGTGGATTTAAACCTTTAAGGTTCTTAACAGTCCCTACAAATGTACAGATATGCAAA
TTTCATAGCTCAATAAAGAACTCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGFVRVYSLPGRENYSSVDANGIQSMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLPFAIKEVGFPRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAPLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRES PNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

[illegible]

GGCGGCGCTCCCGCACC GCGCGGCCGCGCCACCGCGCGCTCCCGCATCTGCACCCGCGAGCCG
GGCGGCGCTCCCGCGGGAGCGAGCAGATCAGTCGCGGCCGCGAGCGCAACTGGTCCGACTCG
GGCGCGCGGCTCGGGCGCGCAGAGCGGAGATCTGACGGGCTTGGGGCGACCCCTGCTGTGCTCG
TGCTGGCGGCGGCGGTCCCCACGGCCCGCGGCCGCTCCGACGGCGACCTCGGCTCTCAGTCT
AAGCCCGGCCGCGCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTATGAGGAGCACGACGACAAATTTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTTAAAGCATCATCAGAAGTGAACCTGCGCAAACTACTCCGAGCTAT
CAAAATGAGACCAACACAGACGAAAGGTTGGAATAATACATCCATGTGTCACGAGAA
TCACAAGATAACCAACAACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCAATCTG
TGGGAGCAGGAAGAGGACGAGAGGAGCCAGGATGCATCATCGACGAGGACTGCGGCGCCAGC
ATGTACTCGCAGTTTGCAGCTTCCAGTACCTGCGACGCCATCGCGGGGCGAGGAGTGCT
CTGCAACCCGGGACAGTGAGTGTGTGGAGACCACTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACACGGGCGAGCATGGGACCATCTGTGACAACTGACAGGGAGTCCGACCGGGGCTG
TGCTGTGCTTTCAGAGAGGCTGTGTTCCCTGTGTGCACACCCCTGCGGTGGAGGGCGA
GCTTTGCCATGACCCCGCGAGCGGCTTGTGCAGCTCATCACTGGGAGCTAGAGCCTGATG
GAGCCTTGACCGATGCGCTTGTGTCAGTGCTCTCTGTGCACGCCCCACGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCTGTGGGGAGCCGTGACCAAGATGGGGAGATCTGTGCC
CAGAGAGGTCCCCGAGATGAGATGAAGTTGGCAGCTTCATGTGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAAGAGGAGCTGTATGAAGAGATGGCGCTGGGGGAGCTCGCGCTGCCCGCCT
GCATGCTGAGGAGGGGAGAGATTTAGATCTGGACACAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTAATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACAGGCTTGTCTCTCA
TCTTCTTCCAGTAAGTTTCCCGTCTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTTCAGC
TCCCCCGAGCTGTCTCCAGGCTTCCAGATCTGGTGTCTGGGAGATGCAGCAGGGTTAAATC
TGCAGGAGCAGTTTGCACCCCGCTGCAGATATTTGGCTGTTTGTCTACCACTGAGCTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTTGTTTGGGGAGGAGATGGAACAAATGTGG
AGTCTCCTCTGATTTGTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACTCAA
CCTGCGCAAAATGCAACAAATGAATTTCCAGCGAGTCTTTTCCATGGGCATAGGTAAGTGT
TGCCTTCACTGTGTGTGCATGAGAAATGTCTGTTCACTCGTCATATCATGTGTTTATTCATCC
ACAGTGTGTGTCTCACTCTTCACTCTGTGTCAGGCGAGCATTTTCATATCCAGATCAATTC
CCTCTCTCAGCACAGCTGGGGAGGGGGTATTGTTCTCTCTGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAGCTGCTTGGCCAGTCCACACAGCATAGTGAAGACAGCAGTGTTCAT
CTGTTTGTGACTCTAAGCTCAGTGCTCTTCCATACCCCAACAGCGCTTGGTGCCACCAA
AAGTGTCTCCCCAAAGGAGGAGGAAATGGGATTTTCTTGAGGATGCATCATCTGGAATTAAG
GTCAAACTAATTTTCATACCTCTAAAGTAAACACTGTGTAGGAACAGCAGTGTCTTCA
AGTGTGGGGCAGCCGCTCTTCTAATGAAGACAAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTTAGTAACTTTGAAAGGTTATATGACTGAGGCTAGCATACAGCTTAACTCGCAGAAAC
GTACTTAGTGTAATTTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCA
TGAAGACAATATCAACACGTGGAGAAATCAAAACCGCAGGGCTGTGTGTAACATGTGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCATCCACAAATGATGTTTTCAGGTGTCA
TGGACTGTTGCCACATGTATTTCATCAGAGTCTTAAAGTTTAAAGTTGCATGATGATTGTA
TAGCATGTCTTTCTTTGATGTTTAAATATGTATAAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTTCAACTCGCAAAAAAATAAAAAAATAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLSAVEEMEAEBAKASSEVNLNLPSPYHNETNTDTKVGNNITIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQEELEDLERSLTFEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

2 3 4 5 6 7 8 9 10 11

JAMES

AAAAA

FIGURE 86

MRLLVAPLLLAUVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQLQSNISIVRVDQSELGYLANLTELDLSQNSFSDARDCCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDNMFRPLANLRSVLVAGMNLREISDYALEGLQSLSELSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNMEELVSIKFAVLNLP
ELTKLDITNNPRLSFIHPRAPHHLPMETMLNMLNLSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRPIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSPFPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGRRPLPPAWAFWGSAPSVRVY
SAPLVLPWNPGKRLPRSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 88

MRQTIKVIKFILIIICYTVYYVHNKFDVDCITVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIIPPSIAQLTGKELWLYHTAAKIEAPALAFLENLRAHFKFTDIKRIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIIDLKDNNLKTIIEIISFQ
HLHRLTCLKLWNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCKRLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRAHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGT**CATG**GAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACCTTTGAGGAAATGGGC
CCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACTGGGTT CAGTTATGTGAATGGTAGTGGTGCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCTCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATT CAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCTTGGGTGATTCTGGATCTCCCTGTTGATTGCGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAAGTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATT CACACAGAGCCACCTAGTTTGTCTTTGT CAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGT CAGGAGGCCTG
GGTGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCCTAAATCTTTGAAACATCTGCTTTTGTCAAGTCTTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAA**TAG**GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAATATTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLWSGPLYLYSMSLLEDKGLAEVSKVAEQVLNAVKNGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRLQRDALS
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMCQEAWVRKLKWPFLPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMLKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCGCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQSSLRLW
DSHVCVGSLLSHRWALTAACHFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSN
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGCGAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGCCCTCATCCTCTCTGGCAAAATGCAGTTACAGCCCCGAGCCCGACAGCGGAGGACGC
 TGCCCCCAGGCTGGGTGTCCCTGGGCCTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGGATCCAG
 CTCTCCTCAATACGGAATAACCTGACCCTAGAGAAATGTGGCTGATCTGGTGAGGCCATCCC
 CACTGACCTCCACACGGTGCAGAAATGGCTCTTGGCAGCCGGAGCCCAAGAGTGCCATTCT
 GTGATCACACAGGACTTTCTGACTGTCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC
 ATCCCTACCAGCTTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
 TTTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCCT
 GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCACAAAGACGTGG
 GCTCTGGCACCGACAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACACAGGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCACT
 ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCTGCACTGGCTCATGTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA
 AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCCTGCTCTTCGCTCAGGTGACAGT
 GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCCTCATCAAAATGAAA
 TTGTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCCTTCATACCAGGAG
 GAAGCTGTAACGAAGTTCTTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
 CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTTCTGATGGCTACTGGGTGGTCAGCAACA
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTGTTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAG
 GCTCTACAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTCTGTC
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAAACAGGC
 TGGGGAACACCAACTTCCAGCTTTGCTTGAAGACTCTACTCAACCCCTGACCCTTTCCTATC
 AGGAGAGATGGCTTGTCCCTGCCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCCCCTGTG
 GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
 TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATATCAGGTCTCCCTACT
 CCTGCCTTAGATTCTCTCAATAAGATGCTGTAACCTAGCATTTTTGTAATGCCCTCTCCCTCCGC
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTGTATACAGACTCTGTGCACTA
 TTTCACTTGATATTCATCCCCAATTCAGTGCAGGAGACCTCTACTGTACCCGTTTACTCT
 TTCTACCTGACATCCAGAAACAATGGCCCTCCAGTGCATACTTCAACTCTTTGCTTTATG
 GCCTTTCCATCATAGTTGCCACCTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG
 ACTACTCTTGCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATGTC
 TCATTTGTAGATTTTTGTCTTCTCTCAGTTTACTCATTTGCCCTGGAAACAAATCACTGACA
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA
 TGTAACAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEFDQRRTLPPGWVSLGRADPEEELSITFALRQQNVERLS
ELVQAVSDPSSPQYGYKYLLENVADLVRPSPLTLHTVQKWLLAAGAQQCHSVITQDFLTCLWL
SIRQAELLPLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPSSYFNASGRAYPDVAALSDGYVWVSNRVIPIWVSGTSASTPVPFGGILSLINEHRILSG
RPPLGLFNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVGTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCCCACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTCTC
TTCTTTCTGCTCTGTGTGTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCTCCCTGTCGTCTTGCCCCAGTCTACCCCTCAATTTAGCCAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCATAAGGGAAC
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTCAAGCATTTTTGGGAAGGACTTCTGCTCAACTACCTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCTGGTGGCAGAGAAGCATGTCCCTCAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA
ATTTCAAGTGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTC
TGGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG
GCACCAAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATGTTTTTTGTCAATTGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACCTG
CTTTGTGTATCATATCATATATCATTAAAGCAGTTTGAAGGCATACTTTGTCATAGAAATAA
AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTTGATTTTTTATTTCATCTGAACCTGTTTCAAAGATTTATATTAAATATTTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGTGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCAGAAAGGTGGGTGTTGCCCTGGGTGGAGC
CCCACCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCCTACCTGATGCCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTTGC
CCCACCTCAGACCTTGCAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCGG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGGCGGCTCGGGCGGTTTCCCCCGCTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCGACCCGCCCCGAC
GGCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCGCCCCCAC
GACTTCCGCCCCGCCCCGGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT
CTCCAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTLLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPIITEDMLCAGYLEGERDACLGDGGGGLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTCTGATGCTTCTGCTGCCGCTACTGCTA
 CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
 GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCAGCGCCTCAGACATGCTGCACATGA
 GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
 AACAAGGAGCGCGGGCGCCGCGGCAGAAATCTGTTGCGCATCACAGACGAGGGCATGGACGT
 GCCGCTGGCCATGGAGGAGTGGCACACGAGCGTGAGCATTACAACCTCAGCGCCGCCACCT
 GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
 GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
 GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
 CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCATCGGAAGC
 CCGGAAGATGCTCAGGATTGCTTACCTTGGTAACTGAGGCCCATCCTTCCGGGCGACTGA
 AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
 TGGTAACAGAGGTTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGTGTGGAACCCAGGCC
 CCAACTTCCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
 AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
 CCTTCCCCAAATCGACCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA
 AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
 GGAACCTCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTG
 AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACATGGAC
 CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCTCAATACCTCTGCCACCGCCTAA
 TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGACAGAGGGCCCTGACA
 AGCCTAGCGTTGTGTACAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCTGGGA
 CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
 TGAAGAGGTCAGCTGTCTCCTGTCTATCTTCCACCCCTGTCCCGAGCCCTAAACAAGATA
 CTTCTTGGTTAAGGCCCTCCGGAAGGGAAGGCTACGGGGCATGTGCCCTCATCACACCATCC
 ATCTTGAGGCAACAAGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
 GGGCCACACCTCTCTGCCCCCTCCCTCCTGAGTCTTGGGGGTGGGAGGATTTGAGGGAGCT
 CACTGCCTACTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCCTG
 TGTAAGTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
 TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAACCT
 GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGQVEETNIELLVCNIEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEAEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLLPPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAGTGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAAATCGGTTCATCTCCAAAGTTATGSGTGAGCGT
 ACTTCTGTGTTCTCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACCTTAAGTGCACAAACAGATTATCTTTCAT
 CAAGGCAAGTTCATGAGCACCTTCAAAGCCTTGGAGAAGTGAAACTGAACAAACATGAATGGAGACCATTC
 AAATCTGGGACGACCTCTGGGCAAAATATTAACATTTCTCCTTGGCTGGAAACAGAGATTTGTAATATCTCCCTGA
 ACATCTGAAAGAGTTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTACAGAGCTCCAAAGTCGATT
 TCCAGGCCCTACAGCTCAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAAACCTGGGTATTTTGACAA
 TTTGGGCCAACACACTCTTGTGTGTTAAAGCTGAACAGGAACTGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAA
 GCCCCAAGTGCACACTCTCGAATTGAACCGAAACAGATTAATAATGTAGATGGACTGACATTTCCAAAGCCTTTGG
 TGCTCTGAAGTCTCTGAAATGCCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAA
 CATGGAAATTTTGAGCTGGACCAATAACAACTTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGTGTATGTCT
 GCAGCAATTTCACTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCTGGGAGTTCTGCCAGGAAGCTCAG
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATAC
 ACTGCACATTTGGGAACAACAGAGTCAGCTACATTTGCTGATTGTGCTTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGATCTGAAGAACAAATGAAATTTCTGGACTATTGAAGCATGAATGGTGTCTTCTCTGGGCTTGACAAATGAG
 GCGACTGATACCTCAAGGAAATCGGATCGTCTTATTACTAAAAAGCCTTCACTGGTTTGGATGATTGGAGCA
 TCTAGACCTGAGTGACAAACGCAATCATGTCTTTACAAGGCAATGCAATTTTCACAAAATGAAGAACTGCAACAAT
 GCATTTAAATACATCAAGCCTTTTGTGCGATTGCGAGTGGCTGAGTAAATGGCTCCACAGTGGGTGGCGGAAACAACTT
 TCAGAGGCTTGTAAATGCCAGTTGTGGCCATCTCAGCTGCTAAAAGGAAGAAGCATTTTGTCTGTAGCCGAGA
 TGGCTTTGTGTGTGATGATTTTCCCAACCCAGATCACGGTTCAGCCGAGAACACAGTGGCAATGAAAGGTTT
 CAAATTTGAGTTTCATCTGCTCAGCTGCCCAGCAGCAGTGATTTCCCAATGACTTTTGTCTGGAAGAAAGACATA
 GATGCTCATGATGCTGAAGTAAATTTATGCACACTCCGGGCCAAGGTGGCGAGGTGATGAGGATATACCA
 CATCTCTCGGCTGGCGAGGTGGAATTTGCGAGTGAGGGGAAATATCAGTGTGTGATCTTCCATCACTTTGGTTC
 CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCAGCCGCCAGATAGCCTGGCAGAGGA
 TGGGGGACAGACTTCCCAGCTGCACCGGAGAGAGCGCATGCTGTGATGCGCCAGAGATGACGTGTTCTTATCGT
 GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCAACAGCTCAGAAACAGTGCAGGAAGTATTTACAGAAATGC
 AACTCTGACTGTCTAGAAACACCATCATTTTGTGGGCCACTGTTGGACGCAACTGTAAACCAAGGAGAAACAGC
 CGTCTTACAGTGCATTGTGCTGGAGGAGCCCTCCCTCTAAACTGAACCTGGACCAAGAGATGATAGGCCATTTGGTGT
 AACCGAGAGGCACTTTTTCGAGCAGGCAATCAGCTTTCTGATTATTGTGGACTCAGATGTTCAGTGTGCTGGGAA
 ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCTCAGCTGTGATCCCCACTCAAC
 CTCGCACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGAATGGGCCACTGTGGGTGTCTGTATCATAGC
 CGTGGTTTGTCTGTGTGGTGGGCACTCACTCGTGTGGGTGTGATCATATATACCAACAAGCGGAGGAATGAAGA
 TTGCAGCATTTACCAACACAGATGAGACCACTTGCACAGCATATTCCTAGTATTTTGTCACTTCAGGGAACGTT
 AGCTGACAGGCAAGTGGGTACGTGCTCTCAGAAAGTGGAAAGCCACCACAGTTTGTCACTCTCAGGTGTCTGG
 ATTTTCTTACCAACAACATGACAGTAGTGGGACCTGCCATATTGCAATAGCAGTGAAGCTGATGTGGAAAGCTGC
 CACAGATCTGTTCTTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGGAAGGAAATGTGTATGGCTCAGA
 TCCTTTTGAACATATATACAGAGTTGTGACTCTGACCCAGAAACAGTTTAAATGGACCACTATGAGCCGAGTTA
 CATAAAGAAAAAGGAGTGCTACCCATGTCTCATCCTTCAGAAGAACTCCGCGACAGGAGCTCAGTAAATATGTC
 GTGGCCTTCAATGTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTG
 TCTAAACAAGTCTCTTTAGATTTTTAGTGCAAAATCCAGAGCAGCGTGGTTGCTCGAGTAAATCTTTCATGGG
 TACCTTTGGAAGGCTCTCAGGAGACCTCACTCATGATGCTTATCAAGCTTTGGACAGCCATCAGATTGTCAAGCC
 AAGAGCCTTTTATTGAAAGCTCATTTCTCCAGACTTTGGACTCTGGGTGAGGAAGATGGGAAGAAAGAGGAC
 AGATTTTCAGGAAGAAATACATTTGTACCTTTAAACAGACTTTAGAAACTACAGGACTCCAAATTTTCAGTCT
 TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAAACATCACTCAAGTCAAGTGAACCTTTTATTA
 AAAGAGAGAGATATTAATGTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGAT
 GACCAAAATTAACAAAGTTATGAAAAATTTTATATCTGGGAATGATGCTCATATAGAATACCTTTTAAACATA
 TTTTTTAACTTTGTTTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAATCATGATTATTTATGATTT
 TTATAATGCCAGATTTCTTTTATGGAAAAATGAGTTACTAAAGCATTTTAAATAACTACCTGCTGTACAACTTTT
 TTAATAGAAGTTACTTCAATATATTTTGACATATATTTTAAATAAAATGTGTCAATTTGAA

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FIGURE 102

MVDVLLLFSLCLLPHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSA
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNI SELQTAFPAQLKLYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLNLRNRIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNTLFTITKGWLYGLLMLQELHLHLSQNAINRISPD
FCQKLESLDLTFNHLRLDDSSFLGLSLNTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDQLKWLPPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLISFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLEAQQ
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVMNLPSTFKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTLVLETPSFLRPLLDRTVTKGETAFLQCIAGGSPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVSDSDVSDAGKYTCMSNTLTGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVIIVAVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNLFPADIPSYLSSQGTILAD
RQDGYVSSESGSHQFVTSAGGFLLPQHDSSGTCCHIDNSSADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSDPDRTVLMDHYEPSYIKKKECYPCSHPEESCSERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYFLKAHSSPDLDGSEEDGKERTDFQEEHNICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTCTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
 AAGGATGCGAGGACCGAGCTTCTCCTGGAAACCGAACCGCATGATGTTGCGCAAGAGAGGAGAAC
 GAAGCTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTTATATGTCACACAGGGAGCATCAAGATGAAA
 TAAACAGAGTTAGACCCCGGGGGTGTGTGTTCTGACATATAATAATCTTAAAGCAGCTGTTCCTCCCTCC
 CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAGAAAAAGTAGTGTTCATTTTCTC
 TATAAAGGAGAAATGAGCCACAGGAGATATTTTGGAAATGAAAGTTTGGGGCTTTTGTAGTAAAGTAAGAACT
 GGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAGAGAAA
 TTTTCAGAGAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGCAGCAGCTTGGGA
 TTTGTGCTTATGTTGACTAAATTTGACGGATAATTGTCAGTTGGATTTCCTTCATCAACCTCTTTTAAAAAT
 TTTTATTCCTTTGGTATCAAGATCATGCGTTTTCTTGTCTTAACCACTCGGATTTCCATCTGGATGTTGCT
 GTGATCAGTCTGAATAACAAGTGTGTTGAATTCAGAAGGACCAACACCCAGATAAATTATGAATGTTGAACAAGAT
 GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGTCT
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGGCTCAGACCTGCCCTCTGTGTGCTCCTGCAGCAA
 CCAGTTTCAGCAAGGTGATTGTGTTGGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
 GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAAATCCT
 ACAGTTGAGTAGGAACCATACAGAACCATGAAATGGGGCTTCAATGTTCTGGCGAACCTCAACACTCTGGA
 ACTCTTTGACAACTGCTTACTACCACTCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
 GCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAACTCTCTTTCGCGCGACTAGACTTAGG
 GGAATTGAAAAAGACTTTCATACATCTCAGAAGGTGCTTTGAAGTCTGCTCCAACCTTGAGGTATTGAACCTTGC
 CATGTGCAACCTTCGGGAAATCCCTAACCTTCACACCGCTCATAAAACTAGATGAGCTGGATCTTCTGCGGAATCA
 TTTATCTGCGCATCAGGCTGGCTCTTTCCAGGGTTGATGCACTTCAAAAACTGGGATGATACAGTCCAGAT
 TCAAGTGATTGAAGGAAATGCCCTTTGACAACCTTCAGTCACATAGTGGAGATTAACCTGGCAACAATAATCTAAC
 ATTACTGCTCTGACCTCTTCACTGCTTCACTGCCCTTGACATCATCTAGAGCGGATACATTTACATCAACCCCTTGAACCTG
 TAACCTGTGACATCTGTGGCTCAGCTGTGTGGATAAAGACATGGCCCTTCGAACACAGCTGTGTGTGCGCGGTG
 TAACACTCTCCCACTCTAAAGGGGAGGTACATTTGGAGAGCTCGACCAAGATTACTTCATGATCTGCTCCGSGT
 GATTGTGGAGGCCCTCGACAGCTCAATGTCTACTGAAGCATGGCAGCTGAGCTGAATGTGCGGCTCCACATC
 CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACATGCGGCGTACAAGTGGCGATAGCTGT
 GCTCAGTGATGGTACGTTAAATTTTCAAAATGTAACTGTGCAAGATACAGGCATGTACACATGTATGGTGAATAA
 TTCCGTTGGGAATACTACTGCTTCAGCCACCTGARTGTACTGCGCAACCACTACTCCTTCTCTTACTTTTC
 AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAGGACCAACAGATAAATGTGGGTCCCACTCC
 AGTGGTGCATGGGAGACCACAATGTGACCACTCTCTCACACACAGAGCACAAGGTGCGACAGAGAAAACTTC
 CACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCAAGACTCCAAATCATCAT
 TGGGTGTTTGTGGCCATCACATCATGGCTGCAAGTGTGTGGTCATTTCCTACAAGATGAGGAAGCAGCACC
 TCGGCAAAACCATCACGCCCAACAAAGGACTGTTGAAATTTATTAATGTGGATGATGAGATTACGGGAGACACCC
 CATGGAAAGCCACTGCGCCATGCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
 CACACACACAACACAGTTAAACAATAAATTAATAACAAGTTCAGTGCATGAAACCGTTATTGATCCGAATGAA
 CTCTAAGACAATGTACAAGAGACTCAAACTAAACAAATTACAGAGTTACAAAAAACAAACAATCAAAAAAAA
 GACAGTTTATTAATAATGACACAATGACTGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
 AAAGAAAGAAATTTATTATTAATAATCTATTGTGATCTAAGCAGACAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRAFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRVYLNAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTLSVSWITPNGTVMTHGAYKVRIVLS DGTNLNFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNTVTSLTPO
STRSTEKTFITPVDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNYSYKSPFNHTTNTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

[illegible]

AGCCGACGCTGCTCAAGCTGCACTCTGTTGCAGTTGGAGTTCTTTTCGGTTTCCCTCTCGTGTTTGGGGGCA
TGAAGAGGGCTTCGCGCCCGGAGTAAGAAAGAAATTCAGCCGGCAGCGAGGAGGAGCGCCAGCCGACGCC
GAGGGCGGGCGGTGACCTTCGGTGGAAGTTGTGCCGGGGCCCGAGCGCCGCCCGGCTGGGAGACTTCGGGATAGA
GACCTTAGGCGCGGTAGACCGGCAATAGACGGCGCGAGCCTTCGTCGGCGCGCGCGGGTTGGGGCTGCTGCTGT
CGGGTGTGGGGCGCGCTGGCGGCTGCAGACAGCGCGGTGCGGGGAATCGGGCAGCCCTTCGGGTAGCCGCC
GAGGCGCCATGCCCCCACTACCTGCTCGCTGCCCTGGGGAGCTGCTGGAGTCAGTCTGAAGCGGCTAGCGGCTTC
CCGAGGACCACTCCGCTTCGGGTGCGCTCGCTGGGATTAAGTCAACAAGATATTTCACTCAAGGCAAGTTTC
ATGAGCCCACTCTCAAAAGCTTCGAGAAGTGAACATGAACCAATGAATTGGAGACCACTCAAAATCTGGGACCA
CTGCGGCAAAATATACCTTCTCTCTGGTGGAAACAGGATTTGGAAATACCTCTGAACTCTGGAAGG
TTTCAGTCCCTTGAAACTTTGGACCTTAGACGACACATATTTCAAGCTCCAACCTGCATTTCCAGCCGCTACAC
CTCAAAATCTGTATCTCAAGCAACCAAGATCAATCAATGAACTCGGGTATTTTGACATTTGGCCAAACAC
CTCCTTTGTGTAAAGCTGAACAGAAACCGAATCTACGATATCCACCAGATGTTTAAACTGGCCCCACTGCA
CATCTGCAATTAAGCCGAAACAAATATAAAATGTATAGTAGCATGACATTCAAAGGCTTTGGTGCTTGAAGTCT
CTGAAATTTGCAAGAAATGGATGTAAACAAATATATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCAATCAACCAATCAACAGATTAACCAAGAGTGGCGGCTGCTTACGGCTTGTGATCTGCAAGAACTCAT
CTCAGCCAAATAGCCATCAACAGATGACCGCTCATGTCTGGGAGTTTCGCGAAGAGCTCAGTGAAGCTGACCTA
CITTTCACTCACTTCAAGTTTAGATGATCAAGCTTCTTGCGCTAAGCTTACTAATACTAGCTGACATTTGGG
AACCAACAGAGTCAGCTACATTTGCTGATTTGGCTCTCGGGGGCTTTTCAGTTTAAAGACTTTGGATCTGAAGAAC
ATAAGAAATTCCTGGACTATGAAGACATGAATGTGTCTTCTGGGCTTGACAACTGAGCGGAGCTAGTACTC
CAAGGAATCCGGTTCGTTCTATTATAAAAGCTTCTCAAGTGTGTGGATGTGATGATGGAGACTATGAGACTGAGT
GACAGCGCAATCATGTCTTATCAAGGCAATGCACTTTCAACTAAGAAACAATGCAACATTTGCAATTTAAATACA
TCAGAGCTTTTGTGCGATTGCCAGCTAAATAGGCTCCCAAGTGGGTGGCGGAAACAACTTTACAGAGCTTTGTA
AATGGCAGTTTGGCCATCTCAGCTGCTAAAGAGGAAGCATTTTGTCTGTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCCAAACCCAGATCAGGCTTCAGCCAGAAACACAGTCGCGCATTAAGGTTTCCAAATTTGAGTTTC
ATTGCTCAGCTGCGACGACGATGATTTCCCAATGACTTTTGTCTGAAAAAGAACATGAACTATGCAATGAT
CTGAAATGGAAATATGCACTACCTCGGGCCAGAGTGGCGAGGTGATGGAGATGACCACTCTGCTGGGTG
CGCGAGGTGGAATTTGCCATGGGGAAATATCAGTGTGTCTATCTCAACTTTTGTGTTCTACTCTCTGTCTC
AAGGCAAGCTTGAAGTAAATATGCTTCCCTCATTTCAAAGAACCCATGGATCTCACCTCCAGCTGGGGCC
ATTGCAAGCTTTGAGTGTGCTGCTGTGGGGCCACGAGCCCGACAGCTGCGAGCAAGATTTACGAACTGACATCTGACTGTC
TTCGAGCTGACGSGGAGAGGACGCACTGATGTATGCCGAGATGACGTGTTCTTTATCTGTGAATGTGAAGTAA
GAGGACATTTGGGTATATTTCTGGGCGCACTGCTGCAGCGAATCTTAACCAAGGAGAAACAGCGCTCTTACAGTGC
ATTGCTGAGGAAGCCCTCCGCTGATTTGAGTCACTGAACTGACCAAGATGATGCCATTTGGTGTAAACGAGAGCC
TTTTTCTGACGAGCAATGACGCTTCGATTTGATGTGACTGAGTCTCAGTGAATGCTGGGAATACAATGTGAG
ATGTTCAACCCCTTGGGCTGAGAGAGGAAACGTGGCGCTCAGTGTATCCCACTCAACTGCACTCCCT
CAGATGACAGCCCCATCGTTAGACGTGACGGAGTGGGCCATGTGGGTGCTGTATACAGCTGTGTTGCTGT
TGGTGGGACGACCACTCGTGTGGGTGTCATCATATACACAGAGCGGAGAAATGAAGATTTGACATATTACC
AACCAAGTAGAGACCAATTCGCAAGGATATTCAGTTATTTGTCATCTCAGGGAACCTTAGCTGACAGGCA
GATGGTACGTGCTCTCAGAAATGGGAAGCCACACAGCTTTGTCATATGCTCAGGTCTCAGGCTGTGATTTCCACCA
CATGATGACAGTAGTGGGACTGTCATATTTAGCAATGACAGTGAAGCTGATGAGAGCTGGCCAGATCTGTCT
CTTTGTTCGTTTGTGGATCTCAGGCAAGCACTATGATTTTGAAGGGAATGTGATGCTCTGATCTTTTGAACA
TATCATACAGTGTGAGTCTGACCGACCGAATGCTTTAATGACCACTAGTGGCCAGTATACATAAAGAAAAG
GAGTGTCTACCCATGCTCATCTCTCAGAGAAGCTCTCGGCAAGGAGCTTCAGTAATATGCTGGGCTTCACAT
TGAGGAAGCTACTTAACTACATGTTATCTTCAATGAAGACCTGGATGAAGAAATCTGTGCTTAACCAAGTCTC
TTCTTAGATTTTAGTGCAAACTCCAGAGCGAGGCTGGTTTGCTCGAGTAATCTTCTCAGGGTACTTTTGAAGA
GCTCTAGAGACCTGACCTAGTGCCCTTCAAGCTTTGGACAGCACTCAGATTTGTCAGCGAAGGCTCTTTAT
TGAAGACTCATTTCTCCCGACATTTGAGCTCTGGGTGAGGAGGAATGGGAAGAAAGACAGATTTTCAGGA
GAAATTCACATTTGATCTTTTAAACAGCACTTTAAGAAATCAAGGACTCCAATTTTCACTGTATGCTTTGAGC
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACTACTACCTCAAGTGAACCTTTATTAAAGAGAGGAAGAT
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAGTCTTTTATATACAGTAGAACCAAAATATAC
AAAAAGTTATGAAAATTTTATACCTGGGAATGCTCATATAAGAATACCTTTTAAACTCTTTTAACTTTG
TTTTATGCAAAAGATCATCTAGTAAATTAATGATATAAATCATGATATTTTATGATATTTTATAATGCGAGA
TTCTTTTATTGAAATAGATGTACTCAAGAACTTTTAAATATACTCGGCTGTGACATTTTATAATAGAGTT
ACTTCATTATATTTTGCATATATATTTTAAATAGTGTGCAATTTTAAAGGTAAGAAAAAAGAAAAAAGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGLDLLDCSR
 KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
 LLSLAGNRIVEILPEHLKEFQSLTLDLSSNNISELQTAFPALQLKYLNLNSNRVTSMEPGY
 FDNLANTLLVLKLNRRNISAI PPKMFKLPQLQHLELNRNKIKNV DGLTFQGLGALKSLKMQR
 NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLMLQELHLSQNAINRISPDAWFC
 QKLESLDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSSLKTLDDLKNNETS
 WTIEDMNGAFSGLDKLRRLLI LQGNRIRISTTKKAF TGLDALEHLDLSDNAIMSLQGNAFSQMK
 KLQQLHLNTSSLLCDQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCCDDF
 PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNE LLHDAEMENYAH LRAQGGGE
 VMEYTTILRLREVEFAS EGKYQCVISNHFSSYSVKA KLTVMMLPSFTKTPMDLTI RAGAMA
 RLECAAVGH PAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQNSA
 GSISANATLTVLETPSFLRPLLDRTVTVKGETAVLQCIAGGSPPPKLNWTKDSDPLVVTTERHF
 FAAGNQLLII VDSDDVSDAGKYTCMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
 TVGVVIAVCCVVGTSLVVVVII YHTRRRNEDCSITNTDETNL PADIPSYLSQQT LADRQ
 DGYVSSBSGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSADVEAATDLFLCFFLGSTGPMY
 LKGNVYGS DPFETYHTGCSDDPRTVLMDHYEPSYIKKKECYPCHSPSESCERSFSNISWPS
 HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRRPHLDAYS
 SFGQPSDCQ PRAFY LKAHSSPDLD SGSEEDGKERTDFQ EENHICTFKQ TLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCGAGCCCGCGGAGCGCAGCTGAGAC
 TGGGGGAGCGCGTTCCGCTGTGTGGGCGCCGCTCGCGCGCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
 CTGCTCCAGCAGGCGCGACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTTATCCCTCTTTATATA
 GAAACCTTCCACACTTGGGAAGGACGCGCGAGGAGGAGGCTCATGGTGAAGCAAGGAGCGCGCTGATCTGCAG
 GCGCACAGACTTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGACACGCTGCTGGT
 TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCAACCCCTGCAGGCAACATGGCCAGAGCGCGGTGTGCTGC
 TGCTCTGTGCTGCTGCCGCCACAGCTGCACCTGGGACTGTGCTTGTGCTGGAGGCGCCAGGATTTGGCCGAA
 GTGGCGGCGACAGCTGAGCCCCAGAGAAACGAATTTGGCGAGGAGGAGCGGTGTGGTACTGAGCCCTGAGG
 AGCCCGGCTGGCCAGCGCGGTGAGTGCCTGCCCGAGACTGTGCTGTTCCAGGAGGCGCTGTGGACTGTG
 CGGTATTGACCTGCGTGAGTTTCCGGGGGACCTGCTGAGCACAAACCACTTCTTGCAGAAACCAACGAG
 TGGAAAGATCTACCTGTGAGGAGCTTCCGGCTGCACCGCTGGAGACTGCAACCTGCAAAACCAACCTGATG
 CTTCGCGAGGCTCCAGAGAAAGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAG
 TGACCTTGGCACCCCGCTTCTGCCAAACGCGCTGATCAGTGTGGACTTGTGCGCAACTATCTCACCAAGATCT
 ATGGGCTCACCTTTGGCCAGAAAGCAAACCTTGAAGTCTGTGTACTGCAACCAACCAAGCTGGCAGAGCGCGGG
 TGCCGGAACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTTCATCTGTGTCAGCAACTTCTGCGCCACGTGC
 CCAAGCACTGCGCGCTGCCCTGTACAAGCTGCACCTCAAGAAACAACAGCTGGAGAAGATCCCCCGGGGGCT
 TCAGCAGGCTGAGCAGCTGCGCGAGCTATACCTGCAAGAAACAACCTACCTGACTGACGAGGCGCTGGACAACGAGA
 CCTTCTGGAAGCTCTCAGCCTGGAGTACTGTGATCTGTGCAACCAACCTGTCTGGGTGCTCCAGCTGGGCTGCG
 CGCGCAGCTGTGCTGCTGCTGCTATCTGGAGAAGAAACGCTATCCGAGCGTGGACGCGAATGTGCTGACCCCTTCC
 GCAGCCTGGAGTACTGCTGCTGTCACGAAACAGCTCGCGGAGCAGGCGCTCACCCACTGGCTTCCAGGGCT
 TCAGCGGTGTGACACCGCTGCACTGTACACAAACGCGCTGGAGCGCTGCCAGTGGCTGCTTCCGCGCGTGC
 GCACCTCTCATGACTCTGCAACCAACAGATCACAGGCATTGGCCGCGAAGACTTTCGCAACCACTTCTTCCGAGG
 AGCTCAACCTCAGCTACCAACCGCTCACAGCCCAACAGGTGCACCGCGAGCTTCCGCAAGCTGCGCTGTGCTGC
 GCTGCTGAGCTGTGCGGCAACCGGCTGCACACGCTGCACTGCGCTGCGCTGMAATGTCCATGTGTGGAAG
 TCAGCGCAATGAGCTGGCTGCTTGTGCAAGAGGGGCGCTGGCGGCTATGCTCAGTGTGAGCTGTACTTCA
 CCAACAAACGCTGCGCAGCGCGGCTTGGCCCGCGTGTGCGGCTGGGAGCTCGCCCTCTGCTGAGTGTGGA
 TCGCCGGAATGCGCTCAGCAGAGATCCCGAGGGGCTCCCGAGTCACTTGAGTACTGTACTTGCAGAAACA
 AGATTAGTGTGCGTGCCTGCGCAATGCTTTCGACTCCAGCCCAACCTCAAGGGGACTTTCCTCAGGTTTAAACAAG
 TGGCTGTGGGCTCGGTGGTGAAGTGCCTTCCGAGGCTGAAGCAGCTGCAAGTCTTGGACATTGAAGGCACT
 TAGAGTTTGTGACATTTCGAAGGACGTTGGCGCTTGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGG
 AGGAAGAGGAAACAAGATAGTGACAAAGGTGATGCAAGTGTGACCTAGGATGATGACCGCGGACTCTTTTGTG
 AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCGTGTGCACAGACACACCAAGCTGCACATGAGGCA
 TCCACATGACAGCGCTGACACAGTCTCATATCCCCACCTTCCACGCGCTGTCCACGCGCACACATGCA
 ACACATCACACCTCAAACACCCAGCTCAGCCACACACAACCTCCCTCAAACCAACCAAGTCTGTGCACAC
 CCCCATCACCGCTGCCACGCGCTCTGAATCATGAGGGAAGGCTGTGCCCTTGCCTTGGCACACACAGGCAACCA
 TTTCCCTCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCTGTGCGAA
 CAGCCCTCAAAGCTATGCCACAGACAGCTCTTGGCCAGCCAGAAATCAGCATTAGCAGCTCGCGCTGTGCGCT
 GTCCATCTGCTCCGTCGTTCCCTGGAGAAAGACAAAGGTTATCCATGCTTGTGGCGAGGTGCTGCCACCTCT
 GGAACCTCAAAAGCTGGCTTTTATTTCTTTCCATCTTATGGGAGCAGGAGCTTCAGGACTGCTGGCTGGCC
 TGGCCACCCCTGCTCTCCAGGTGCTGGGAGTCACTGTGAAGAGTCTCTCTGCGCAGCGCTGGCAGGACA
 CAGGCACTTTTCAATGGCAAGCCGAGTGGAGGAGGAGTGGAGAGCCCGCTGGGTGTGCTGGGCGCTTGGG
 CAGGATGAGCAGAGGTGATGGGCTGGGCTGAGCCAGGGAGGAAGGACAGCTGCACTTAGGAGCAACCTTT
 GTTCTTCAAGGCTGTGGGGAAGTTCCGGGTGCCTTTATTTTATTTTCTTAAAGAAAAAATGATAAAAAAT
 CTCAAAGCTGATTTTCTGTATAGAAAAACTAATATAAAAGCATATCCCTATCCCTGCAAAAAA

0903740 071104
 001205 072066

FIGURE 108

MEGEEAEQPAWFHQWPRPGASDSAPPAGTMAQSRVLLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFFPGDLP
EHTNHLSQLNNQLEKIYPEELSRRLHRLLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDMMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLELYLQNNYLTDEGLDN
ETFWKLSSELYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHNS
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMIHLNQITGIGREDFATTYF
LEELNLSYNRITSQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSSVDSAFRRLLKHLQVLDIEGNLEFGDISK
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGCGCGCGCCCTCGCCGCTGCTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGCGAGGGCTGCGGGGTTCCTCGAGACTCTCAGAGGGGCGCCTCCCATCGCGCCACACCC
CAACCTGTTCCTCGCGCGCCACTGCGCTGCGCCCGAGGACCGCTGCCCAATGAGTTTCTCTGGCGCTGGT
GCTGGTATCTCGCTCTACCTCGCAGGCGGCGCGCAGTTTCAGACGGGAGGTGGCCAGGCAAAATAGTGTATCGAT
TGGCCTATGTTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGCGGACAGTGTGACGC
TGTGTGCGAACACGATGCAAAATGTTGATGTATCGGGGCAAAACAGTGTCAAGTGTCTATCTGGTTATGCTGG
AAAAACCTGTAACTCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGCGCCTGTAAAGCACAGGTGATGAACAATTA
CGGCAGCTACAAGTCTACTGTCTCAACGGATATATGCTCATGCGGATGGTTCTGCTCAAGTGGCTGACCTG
CTCCATGGCAAACTGTGAGTGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGGCCATCCCGTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGGCTCCCTGCCCTAGATT
TAGGCAATGTCTCAACATCTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTTGGAGG
CAAAATCAATGTACATAGACATAGACGAATGCTCACTGGTCAGTATCAGTGCAGCAGCTTGTCTGATGTTATAA
CGTACGTGGGTCTTACAAAGTGCAAAATGTAAGAAGGATACAGGGTGTATGGACTGACTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAATGTTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAACTGTTGGTGGCTCCGAAGACACCATATATTCCTCCTATCATTACCAA
CAGGCGCTACTTCTAAGCCAACAACAGACCTTACACCAAGGCAACACCAATTCCTACTCCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACTACAACCCAGAAAGGCCAACACCGGACTGCAACTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACACAGGGTACAGACAGACCTCAGAAACCCAGAG
AGATGTGTTTCAGTGTTCGTGTACAGTGTGTAATTTTGACCATGGACTTGTGGATGGATCAGGAGAGAAGACAA
TGACTTGCATGGGAACCAATCAGGAGCCAGCAGGTGGACAAATATCTGACAGTGTGGCGAGCCAAAGCCCCAGG
GGGAAAAGCTGCAGCTGCTGGTGTACCTCTCGCGCGCTCATGCACTTACAGGGGACTGTGCTGCTGATTTCAGGCA
CAAGGTGACGGGGTGCACCTCGGCACACTCCAGGTGTTTGTGAGAAAACAGCGTGCCACAGGAGAGCCCTGTG
GGGAGAAATGTGGTGCCTGGCTGGAGGCAACACAGATCACTTTCGAGGGGCTGACATCAAGAGCCGAATCACA
AAGATGATTAAAGGGTGTGAAAAAAGATCTATGATGGAATAATTAAGGAATCGGATATATGAGCCTTGAGAAAG
AGAAGACTGAGGGGCAACCAATTCATGCTGTTTCAAGTATATGAAGGTTGGCAGCAGAGGGTGGCGACACAGCTG
TCTTCCATGTACGCTAAGATAGAACAGAGGAACTGGCTAGACTAGAGTATAAGGGATGAGTCTTTCGGCAGG
GGCCATGTTAGAATACTTCATAAAAAAAGAGTGTGAAATCTCAGTATCTCTCTCTTTCTAAAAAATATAGA
TAAAAATTTGCTATTTAAGATGTTAAAGATGTTCTTACCAAGGAAAGTAAACAAATATAGAAATTTCCAAAA
AGATGTTTGTATCTCTAGTAGTATGAGTGAAAAATCTTTAGAACTAAATAAATTTGGACAGGGCTTAATTTAGG
CAATTCCTCTTGACCTCCTAATGAGAGGGATGAAAGGGGAAGAGCCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTCAGCAGTATTAAGAAAAAAGGAAACATTTATTCACAAATGAGAGTATGATGGAC
AGATATTTAGTATCTCAGTAATGTCTTAGTGTGGCGGTGTTTTCAATGTTTCTTCAGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGCTTCAGAG
ATTTTCATCGGGTGCACTTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGTGAGAAAAGAGTGGCCTGCCCC
ACACCGCGAGACCTTCTCTCACTCATCAGTATGATTACAGTTTCTCTTATCAATTTGACTCTCCAGGTTCAC
AGAACAGTAATATTTTGAACAATAGGTACAATAGAGGTCTCTGTCATTTAACTGGTAAAGGCAAGGCTGG
AGGGGGAAAAATAATCATTAAGCCTTTGAGTAACGCGCAATATATGGCTGTAGATCCATTTTAAATGGTTTCAAT
TCCTTTATGTTCAATACTGACAGCTGAAGATGAAAGGGGAAAAATAAGTAAAAATTTTATTTTCGATGCCAA
TGATACATTCGACTAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTAATTTAAAGTTT
CTAAATAAAAAATTTAGTGGTTTTCCAAATGGCTATATAAAAAATTAATTTTGAATAGAACACCTGTATGTAAT

FIGURE 110

MDFLLLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCOYGCDEVVKGQIRQCPSFGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSPARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWWPCKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDQKPRGDVFSVLVHSCNFDHGLCGWIREKDNLDHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRIMHSGDLCLSPRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHWQRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCAATTTGCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCCTTCACAACCTTTCTTTCTTTTGCAACAGGTGCTTGGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGTGAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGGAAATGGAACCTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCTCCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTCTCAGTGAATGGAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTGTGATTGTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAACTACATATATCATTAAAGCATGGGCCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAATATCAACCCACAAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTGCTTTTCCAGATGTTTCTGGTGTTCACAG
ATTTCAAGCAGGTCGTTCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTGACGACATCCCTGCCCAGCAGCAAGACCATCCAGAGT**G**AACCTTTTCATGG
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTATGCAAAATGAACTGCAGGTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTCTTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAA
TGTGGAAACTTTACATTGTTTCGATTTTTCAGCAGACTTGTTTTATTAATTTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAATATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTCAAGGAAAGATGGATTCAATAAATTATTCTGTTTTTGCTTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPFVSEMSDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKYQPYKVIKQK
LEGREPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

[illegible]

CCAAGCGGCGAAATGCGCCCTCCGGGAGCTCTTGCAATTCCTCCTGGCAGTCTCGTGTGCTGTT
 GCTTTGGGTGCTCCCTCGAGCAGCAGGGCGGGAGCAACGTTTCGCGTCATCCAGCCAGAGA
 ACTCGAGAGAACTCTGCTGGAAGGAGACTGGATGATAGAATTTTATCCCCGGTGGTGGCCGCTCT
 TGTCAAATCTTCAACCGGAATGGGAAAGTTTCTGCTAGATGGGGAAGACTCTTAGGTTAA
 TATTGCGAAAGTAGATGTCACAGACAGCCAGGACTGAGTGGACGTTTATCATTAATCTGCTC
 TTCCTACTATTTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
 AAGCACTCATAAACCTTTATAAGTGATAAAGAGTGGGAAGAGTATGAGCCGGTTTCATCAT
 GTTTGGTCAGGTTCTGTTCTGATGAGTAGATGTCAGCACTCTTTCAGCTATCTATGTGGGA
 TCAGGACGTGCCATAACTACTTTATTGAAGCACTTTGGATTGCCAGTGGGGATCATATACT
 GTTTTGTCTTTAGCAACTCTGTTTTCGGAGCTTTATTAGGACTCTGTATGATATTTTGGG
 AGATTGCTCTTTGTCCTTCAAAAGGCGCAGACCAAGCCATACCATAACCTTCAAAAAT
 TATTTATCAGAATCTGCCAACCTTTTGAAAAGAGTGGAGGAGGCAAGAGCGCGGATGAAGAA
 GATGTTTCAAGAAGAAGCTGAAATGAAGAAGGAAACAAACAAAGCTTCCAGAATGTC
 CATAAGCAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCCAGTTTAAATTTTATAG
 TTATCTTAATATATGATTTTGATAAAAAACAGAAAGTTGATCATCTTTGTGGTTTGAAGTG
 AACTGTGACTTTTGTGAATATGTCAGGGTTTCAGTGTAGATTGCTATAAATGAAGAGCTCA
 CATTCAGAACTATAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCAAGTATGATG
 GTTTAAATAGTCTCTTAATTTTGA AAAATCTGTGCCAAGCAATAAGATTTTATGATATTTGT
 TTAATAATAACCTATTTCAGTCTGAGTTTGTGA AAATTTACATTTTCCCAAGTATTGCTATT
 TGAGGATTTAAGAAGATATTTTATGAGAAAATATTTCTCATTTGATATTAATTTTCTCTGT
 TTTCACTGTGTGA AAAAAGAGATATTTCCCAATAAATGGGAAGTTTGCCCATTTGPTCTAAG
 AAATGTGATATTCAGTGA CAATTTCTGTGCTCTTTTAGAGGTATATTTCCAAATTTTCTGT
 ATTTTTCAGGTTATGCAACTATAAAAACCTACCTTACATTAATTAATTCAGTTTCTACACA
 TGGTAATACAGGATATGCTACTGATTTTAGGAAGTTTAAAGTTCATGATATTTCTCTGTATTC
 CAACAAGATTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTTACATTTTATTTT
 CAAATGGATGATAATTTCTTGGGAACATTTTATGTTTGAAGTAACAGATTTTTTTGTGT
 GTTCAAACCTGAAGTTTACTGAGAGATCCATCAATTTGAACAATCTGTTGTAATTTAAAAAT
 TTGGCCACTTTTTCAGATTTTACATCATTTCTGCTGAATCTCAACTTGA AATTTGTTTTTT
 TTTCTTTTGGATGTGAAGGTGAACATCTCTGATTTTGTGCTGATGGA AAAAGCCTTGTA
 TTTTACATTTTGA AATTTCAAGAAGCTTAATATAAAGTTTGCATCTTACATCAGGA AATG
 CATCTCTCTGTATGCTTAAATGTATTTTGTCTCATATACAGAAAGTCTTAAATGAT
 TTTACAGTCTGTAAATGCTTGATGTTTAAAAATAAACATTTTATATTTTAAAAAGCAA
 ACTCTATATTTCTCTGTTGCTCTCTCTGACTGGTAATTTATGTTGGGATTTCAAGGTA AAA
 GTCAGTAGGATGGAACATTTTAGTGATTTTATCTTTAAAGAGCTAGAATACATAGTTT
 CACCTTAAAGAGAGGGGAAAAATCAATAACATCAATCACTGACCATAGCTAGTATGAC
 AATTTCTGTAAATGCCCCCTCTCTTTAGGCTCTGTTGTGTGAATCATTAGATTTTACAG
 TATCGTAATATACAAGTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAAAATTTGTACCATT
 AAAGAGTTTGGATGTGTAACCTGTGATGCCCTAGAAAATATCTTAAGCACAAAATAAACCT
 TTTAAACCTTTCAATAAGCTGAAAAA AAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFIISKWKSEIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPSPKKLLSESAQPLKKVEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQRS LGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

[illegible]

CGCAGTGTCCAGCTGCGGAGACCCGTGATAATCGTTAACTAATTCAACAACGGGACCCTT
CTAGTGTGCCGAAGACCGCACAGCAGTGTGCTAACCCAGTGGGACAGCGGAGTGGGAAGAGCGGCG
AAGTCCCTGGCGCCAGAGCAGTGTGACATCTCCCTCTGTGACCTGAAACTCTGGGTGTGCG
ATTGCTGATGACCTTGGTTTGGTGTCTCGAGCTGTGTGCGAGCGCAATTTCTTCACTCTATTG
GGCACAATGATGCATCTGATTTATGCGAGAAAGAGCTGGTGCACTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAAGCTTTCCAAAGTTAAGAGCTGGGCCAACAAAATGGAAGCCCTTGA
TAGCAAGTGCAGTGTCTGTATGCTTGAGGGCTACTTGCGCTCACCTGTGTAATGCCACAACATGG
TGAAGCGGCTAAACAAGACAGATGGCCCTGCGCTGGAGAACCTTGTCTTGAGGACTCAGTGCAC
GGTTTTATCGCCAACTCTCTGTGTGACGCGCAGTTCCTCCCACTGATGAGGACGAGTATAGG
AGCTGCGCAAAAGCCCTGATGAGACTCTCAGGACACATACAGGCTGGCCACCGGCACAATTTCCA
GAGGGAACCTTCAGGAAACAAGTACCAGGCAATCTGAGTGTGGATGACTGCTTTGGGATG
GGCCCTCTCGCCCTCAATGAAGGGGACTATTATCATACGGTGTGTGTGGATGGAGCAGGTGCT
AACGACAGCTTGATGCGGGGAGGAGGCCACAACCAAGTACAGGTTGCTGGACTACCTCA
GCTATGCTGTCTTCAGTGTGGGTGATCTGCACCGTGCCCTGGAGCTACCCGCGCGCTGTCT
TCCCTTGACCCAAGCAGCAAGCAGCTGGAGGGAATCTGCGGTACITTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACCTTAAACAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGACA
TCTATGAGAGGCCCTGTGGACTACCTGCCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGG
GAGGTGCTCAAACTGACACCCCGTAGACAGAGAAGGCTTTCTGTAGGTACACCATGCGGCAA
CAGGGCCCCAGAGCTGCTCATTCGCCCCCTTCAAAGAGGAGGACAGTGGGACAGGCCGCA
TCGTCAAGTACTACAGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CTCAAACCTTGACAGGACCCAGCTTCGTGTGATGAGTACCAAGACAGGAGTCTCACCTGTGCGGACGTA
CCGGGTTTCCAAAGCTCTCTGGCTAGAGGAAGTATGATACCTGTTGTGGCCGATGAGTAATC
GTCCGATGTCAGCATATCAACAGGGTTACAGTAAAGACTGTCAGAATTTGTCAGGTTGCAAAAT
TATCGAGTGGGAGGACAGTATGAACCCGACTTCTGACTTCTTAGGCCACCTTTTGAACGCG
CCTCAAAACAGAGGGGGAATAGGTTAGCGACCTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGTGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTTGGCCATGAAGAAGGATACAGCTGTG
TTCTGTGTAACAACCTCTTGCGAGCGGGAGAGGTGACTACGCCAACAGACATGTGCTGCTGCC
TGTGCTTGTGGGCTGCAAGTGGGTTCTCAATAAGTGTGTTCCATGAAACAGGAGCAGGAGTTCT
TGACACTTTGTGGATCAACAGGAGTTGACTGGAACCTCTTTCTGTGCTCTCCCTCTCTGCTGTC
CTTACGCCATGTCAACGTGACAGACACTTTGTATGTTTCCTTTGTATGTTCTCTTACAGGCT
GATTTTGGAGAATGAATGTTTGTCTGAGCAGAGGGAGACCATACAGGCGCACTCTGTG
GTACTGAAGTCCAGCCTTTCCATTGACCGCTGTGCCATCCTGTGCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTTGCGAGATGTTTACGTGAACCAAAAGTCTTGATACCTTTTACATGTTGTTGTTTTAT
GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAATGTGCTCCATGAGCAAAAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQROFFP
TDEDEIGAALKMRLQDLYRLDPGTISRGEPLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVLDYLPEDVYESLCRGEQVKLTPRRQKRLF
CRYHHGNRAPOLLIAPFKEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRMRQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYSMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYL
TRHAACPVLVGCKWVSNKWFHERGQEFLLRPGSGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 118

MRLSSLLALLRPALEPLILGLSLGCSLSLLRVSWIQEGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDDEDFKPRIVPYYRDPNPKPYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQGRAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPFVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALLETALQLNRRYQPRLRFQKQRLNNGYR
RFDPARGMEYTLDLLLECCTQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVQLVLPPL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTVMVTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPFSPPGADPSRGAPIGGGRFDRQASAEGCFFYNADYLAA
RARLAGELAGQEEEEEALGLEVMDVFLRFSGLHLFRAVEPLGLVQKFSRLRDCSPRLSEELYHR
CRLSNLEGLGGRQAQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTAAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAAAAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAGCAG
AGTTCTTCAGTTCGTAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTCTATTAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAATGGTTCGACAATGACTGAGAAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCAATTATTTGTAGTAGTAACACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAAAACACATGAACATTGTAAATG
TGTTGGAAGAAGTGTTTTAAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTTCTAAATTATGAACATTAGAAATCTGTGGGGCAGATATTTTGCTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACCTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTCGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFrvYCIILVKPKDVS LWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCP EQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFN
KSVGLS I KEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFPHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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[illegible]

FIGURE 122

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCPLNWEYFQSSCYFFSTDTISWALSCLKNCAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

[illegible]

GAGGATCAACAAGCCGGCGCTCGCGCTCGGCCCTCAGCAAGACCTTCAGCAATGGCGCGCTAGGCGCGGCACCGCGGAC
 TCGCGCTCTCGCGCTCGCTCGCTGACTGCTTCTCTGCTGCTGTTTTCAGGGCGCTCTGATAGAGGGCTGTAAATCT
 TCAAATTCAGCAACATCGAACCCAGCTGGTACAGGAATTTGAAAGTGTGGAACTGTCTTGCAATCATTAACGGATTCCG
 AGCAAAAGTGCACCCGAGCAATCCGATCCGATGGGAAGAAATTCAGAGTGAACAAACACCATATGTGTTTTTGCAACACAAA
 TTTCAGGGAGATCTGGCGGCTGTGTGCAGAAATCTGGGGAAGACATCCCTGAAGATCTGGAATGTGCACGGAGAG
 ACTCGACCTGTTATTCGCTGTAGGTGTGTGCTGCAGAAATGCAAGCCAGGAAATGATGAGATTTGTATCGAGTTAAAT
 CTGTGCAAGTGAAGGCATGACACCTGTCTGTAGATGTGCGAAGCGTGTACAGTAGGCGCAAGTGGCAACATCG
 ACTGTCGAGGAGATGTAGGGGCAACCCCCGGGCTACATACAGCTGATATCGAATGATGTACATCGCCACGGAT
 CCAGAGCAAAATCCGCAATTTTGCAAATTTCTTTTCCATATTAATCTGAAACAGGCATCTTGGTGTGTCTCATGCTCT
 TTTCAACAAGCAGCATCTGGGCGACTATCTGCGATTGCTTCAATGACGACGCTTACGCCAGTGTGGAGGACGAGG
 AGATGGGAAGTCTATGACCTGAAATTTGGCGAAATTTGGGGGGGTTTGTGTTGTCTGCTGTCTGCTGCTGGCCATCA
 TCACGCTGGGGATCTGCTGTGCATACAGACGTGGCTACTTCATCAACATAAACAGATGGAGAAAGTTTACAAGA
 ACCAGGGAAGAACAGATGAGAGTTAACTACATCCGACATGACGAGGAGGCGCATCTCAGACAGAAAGTCATGTGTTT
 TGATCTGAGACCGCGGCTGTGCTGTGAGGCGACAGAGCGCAGCTGCACATACCTGTCTGTGAGCAACCTCCTGTACA
 GCGCAGCAGAGCTGTGACTGCAGCAGAGCTAGACATCTTACAGAAAGCTTTTCGTTTGGCAAGTGTGACCA
 CTAATCTTTCTACTTAAACAGGCATCAATGATAGAAATTTCTTCAAGTGAAGCCCGGTAAATATTAACCAACCA
 GGAAGCGAAATCGGGTGGTTCATCTGAGTTGGGTTCTTAATCTGTTTGTGGCTGATTCGCGATTAATTAAGTATAGG
 GTGATCTTAAAGAGTTTGTCTCACTGAAACCGCCGCTGTGGCCGCTGTGAAGCCGAGCATTTCCACCTGTGCTGTT
 CAGAGCGCCACAGACACCATGTAGATGTGCGAGGTGCTGTGACAGCAGCAGCAGCGCATTCGCGCGGGAACTCA
 GAAAGGGCTTTTACACAGCAGCTTACTTATCTCGGCCACAGACACCCGAGTGTCTTCTTAAAGGCTCTGCT
 TGATCGGTTGTGTCAGTGTACTTGTGGAAGAGCTTTTGGATGAGCATTTGTGTAAGAACACCAAAATCAGGAAG
 ACTTAATTTGGTTGTGGAAGAGTGTCTGCTGAGGAACCTCTGTTCCCAACAGGGGTGTAGGATTTAAGGAAGA
 GCTTTTCTCTTAGGCTAAGTGGAAATGTGATCGAAATGCTTTCTATGGGCTGTCTTATTTATAAAATTT
 TACATCTAAATTTTGTCAAGGATGTTATTTTGATTTGTGTAAGAAAGAAATTTCTAATTTAAACTGTAAATATTTGT
 TATACAATGTAAATAACTATTTTAAAAAAGTCAACTGTAGAGATTTCAAGCTGTACAGTGTAAAT
 TGGAAATATCAATAATTAAGATATTTTACCAGGAATCCTCTCATGSAAGTTTACTGTGATGTCTTTCTTCTTCT
 GCAACAAGTTTGTAGCTTTTCTACAGGAGCACTACTGCTACACATGAGACCATGTGCTGTAGGAACCTT
 TAAAAATTCAGTGTAAAGCATTTGAAATCAGTTTGTGATCTCTTCAAAAGAACTCTCAGTTAGCTTTGAACT
 GCGCTCTCTCGATGATAGCATTAGCAGCTCTGACCCAGGCGCCACCGAGCTCCAGATGTACATACATAGATG
 CAGTCACTGCTCTGCGGTTGTGCGACGAGCGCCCGGCTAGCTCATGTGTCTGCGCTGTCTGCGCAGAGAGCGCT
 GCGATCTTGTGGCGCTGTGACAGTGCGCTGTGTCCGATGAGCTTTACTACAGTGCGCCCTTGCTCTATCCAGCAGC
 TCTCAGGTGGGACCTGCGGAACATGTGTGTTCTTCATGTAGCTCCGAGCTTTGGGCTCCTGTACAAGACCTCT
 TTTGGTATGTAGTGCTCTCAAAAATAGGCGCCCACTAGCTATTTTCTTTTAAAGTTTGTTTAAATTTATTTGT
 AGATTTGTCTAAGGCGCAAAGCAATTCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAATGAT
 CCGATCTTCTCTTTTGCACAGAGAAGCACCAGCGACCAAGGCTGTGTCGCAATTCAAAACAAACCATGAT
 GAGTGTCGCGCAGTCCAGCCTTTTAAAGAAGCTCAGTGGAGCAGCAGGTGTAAGAGGCTGTGCGGGGAGGAAG
 TGAAGCGCGTGAATCAAAGCAGTTTCTTAATTTTGAATCTTAAATTTTCTCGCGCGGAGACATCTGCTCCCATTT
 TGTGGGGGCAATPAGCAATCATCAGAGGCTGTGTGTTCTCAAGCAGGTTGTCTCAGCTCTACATGAGCGCT
 GCGTGTGTGGAATCAGGACTGAGTGTGTGTAAGCAGAGGAGCTGCTGGAAGAGGAGACTCCATCTGTGTGCTGGA
 GAATGGCTCTCACTACTCACTTGTCTTTCAGCTTCCAGTCTTGGGTTTTTATATCTTGACGCTTTTCTTT
 TTTGTCATCATAGAGCTGTGTGACTTTTTTGTATTTGTGTAAGCACTTTGCGCGAGCGCGCTGTGCAGAGGCA
 GGAATGCTCCAGCATGGCTGTGCTGCTCCCTGTGTCTGCTGATGCTCATGTCATCTGGATGTATGACATCAAGTTCT
 CTTCACTCATGCGCACTGTGTTGAGAGAGAGGTGGCTCCCACTCCAGGTTGGGAATTCAGGCTCGAGCTCTCT
 TCTGGTGTCTAAGTGA TAGGTTAGCTTTATGGCCCTTCTTATACCTTAAACCTTTACATATGAGTGCCA
 TGGAAACAGGATCTGAAAGAAATGAGAGAGATGAAGATGATCTGGGAAGTAGCTGCTTAACTAGACATGACATGA
 CGGAAAGCGAATCTCGTGATTTTAAGATATGAATGTGACTCAAGACTCAGGCGCGATACAGGCTGTGATCT
 GCTTTTGGATGGATGTGCTGTGACACAGTGCTACAGACTGTGATCTAACACACGTAATTTGGCATTTGTTTTAACT
 CTATTTTAAAGAGCTTTCAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSKINWVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVCVRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIG
VLVVLAVLALITLIGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267